



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 157724

TO: Patricia Duffy
Location: rem/3b05/3c18
Art Unit: 1645
Monday, March 29, 2004

Case Serial Number: 09/438185

From: Peggy Ruppel
Location: Biotech-Chem Library
Phone: 571-272-2557
REM E01b65
peggy.ruppel@uspto.gov

Search Notes

Dear Examiner Duffy:

The results of your search request are attached.

Feel free to contact me if you have any questions.

Thank you for using STIC services.

Peggy Ruppel
2-2557

Gendore version 5.1.6
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OM protein - protein search, using BW model

Run on: March 25, 2004, 14:10:43 ; Search time 59 Seconds

1733.597 Million cell alignments/sec

Title: US-09-438-185A-1047

Perfect score: 1889

Sequence: 1 VHYCRTLDPKYIKAALKU.....ESTPLYNQEKKYLSGFPEVLCQ 362

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1586107 seqs, 28547505 residues

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: GeneseqP1980s:*
- 2: GeneseqP1990s:*
- 3: GeneseqP2000s:*
- 4: GeneseqP2001s:*
- 5: GeneseqP2002s:*
- 6: GeneseqP2003s:*
- 7: GeneseqP2003bs:*
- 8: GeneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1889	100 0	362	5	ABB90626	Abb90626 Chlamydia
2	1250.5	66.2	259	2	AY35703	Aay35703 Chlamydia
3	237	12.5	429	4	AAE11086	Aae11086 Protein e
4	235.5	12.5	262	7	ADD47706	Add47706 Rat Prote
5	235.5	12.5	262	7	ADD48839	Add48839 Rat Prote
6	231.5	12.5	415	4	AAB11161	Aab11161 PhthAB fus
7	231.5	12.3	444	5	AAM80192	Aam80192 Human Pro
8	231.5	12.3	444	5	ABG95631	Abg95631 Human ova
9	231.5	12.3	466	4	ABG96432	Abg96432 Human ova
10	227.5	12.0	444	4	AAM79308	Aam79308 Human pro
11	226.5	12.0	434	5	AAO17129	Aac17329 Neurone s
12	223	11.8	498	7	ADE60903	Ado60903 Rat Prote
13	223	11.8	498	7	ADE60907	Ado60907 Rat Prote
14	222	11.8	498	2	AAR50185	Aar50185 Rat tyros
15	221	11.7	498	2	AAR56741	Aar56741 Rat tyros
16	220	11.6	497	2	AAR50184	Aar50184 Human tyro
17	219	11.6	497	2	AAR36710	Aar36710 Human Tyr
18	219	11.6	579	4	ABB64882	Abb64882 Drosophil
19	216.5	11.5	484	6	AAG79758	Aag79758 Human hyd
20	216.5	11.5	485	6	AAG79757	Aag79757 Human hyd
21	216.5	11.5	486	6	AAG79756	Aag79756 Human hyd
22	216.5	11.5	490	6	AAG79755	Aag79755 Human hyd
23	213.5	11.3	452	2	AAW25788	Aaw25788 Human phe
24	213.5	11.3	452	2	AY55893	Aay55893 Human phe

AY78593 Human phe
 Abb11909 Protein r
 Add18674 Human dis
 Abi13327 Caenorhab
 Aau10703 Novel hum
 Abb971947 C. violac
 Abb61277 Drosophil
 Abb11186 Drosophil
 Aau30702 Novel hum
 Aae11092 PhthAB fus
 Abp06168 Human ORF
 Abb61194 Drosophil
 Abb65685 Drosophil
 Abp25686 Fungal ZB
 Aab4081 Human pro
 Abb59689 Drosophil
 Add56334 Human pro
 Aaw61848 Amino aci
 Ade54882 Rat Prote
 Ade54870 Rat Prote

ALTGNENTS

RESULT 1

ID ABB90626 standard; protein; 362 AA.

ID ABB90626;

AC XX

DT DT

XX 29-AUG-2003 (revised)

XX 29-JUL-2002 (first entry)

DE DE

XX Chlamydia pneumoniae cp1380 protein, SEQ ID NO:201.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;

XX human respiratory disease; cardiovascular disease; atherosclerosis;

XX coronary artery disease; carotid artery stenosis; myocardial infarction;

XX cerebrovascular disease; aortic aneurysm; claudication; stroke;

XX strain Cw029.

OS OS

PN PN

WO200202605-A2.

XX WO200202605-A2.

XX 10-JAN-2002.

PD PD

XX 03-JUL-2001; 2001WO-IB001445.

PF PF

XX 03-JUL-2000; 2000GB-00016363.

PR PR

XX 11-JUL-2000; 2000GB-0001047.

PR PR

21-JUL-2000; 2000GB-00011983.

PR PR

07-AUG-2000; 2000GB-00012368.

PR PR

18-AUG-2000; 2000GB-00023440.

PR PR

14-SEP-2000; 2000GB-00025583.

PR PR

10-NOV-2000; 2000GB-00025549.

PR PR

22-DEC-2000; 2000GB-00031706.

DR DR

XX (CHIR-) CHIRON SPA.

XX Ratti G, Grandi G;

XX WPI; 2002-154726/20.

XX DR N-PSDB; ABH91284.

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, and for diagnostic purposes.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia

CC pneumoniae (strain CWL029), and ABL9184-ABL91373 represent DNA encoding pneumoniae. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention. (Updated on 29-Aug-2003 to standardise OS field)

Sequence 362 AA;

Query Match Score 1889; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e-182;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHYCERTDPKYIYLKIALRQSLFQLFFONSQLQRAYSTPSYSYRILQKENKEKOALA 60
Db 1 VHYCERTDPKYIYLKIALRQSLFQLFFONSQLQRAYSTPSYSYRILQKENKEKOALA 60

Qy 61 RHKCISLLEFEKKNLFVHJLSLSKRNQRCSTUMAVSTPFENRNLWYRLJSSREFWK 120
Db 61 RHKCISLLEFEKKNLFVHJLSLSKRNQRECSTUMAVSTPFENRNLWYRLJSSRFSTWK 120

Qy 121 YCPRFPLDYLEAFLGILSDFLDHQAVIKKFPELETHFSYVPSGVAPHQYLSIQDRYFPI 180
Db 121 YCPRFPLDYLEAFLGILSDFLDHQAVIKKFPELETHFSYVPSGVAPHQYLSIQDRYFPI 180

Qy 181 ASVNTLDDKDNFSLTPDLIHDLLGHVPNLLHPSSEFPINNGRLPTKVIEVKOALPSKKQ 240
Db 181 ASVNTLDDKDNFSLTPDLIHDLLGHVPNLLHPSSEFTLNMGRLTXVIEVKOALPSKKQ 240

Qy 241 RIQTQSNLIAITVRCFWTFVESGLLENHGRKAYAVLSSPQLGHAFIDNVRVLEL 300
Db 241 RIQTQSNLIAITVRCFWTFVESGLLENHGRKAYAVLSSPQLGHAFIDNVRVLEL 300

Qy 301 DQIIRLPFTNSTPOETLFSIRHFDELVELTSKLEMWDQGLLIESIPLYNOEYKLSGFEV 360
Db 301 DQIIRLPFTNSTPOETLFSIRHFDELVELTSKLEMWDQGLLIESIPLYNOEYKLSGFEV 360

Qy 361 CQ 362
Db 361 CQ 362

RESULT 2
ID AAY35703 standard; protein; 259 AA.

XX AAY35703;

XX DT 17-OCT-2003 (revised)

XX 13-SEP-1999 (first entry)

DE Chlamydia pneumoniae transmembrane protein sequence.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

KW neutralising epitope.

XX Chlamydophila pneumoniae.

XX PN W09927105-A2.

XX PD 03-JUN-1999.

XX XX

XX XX

XX DE

XX Protein encoded by pFUSAB vector DNA insert sequence.

XX XX

XX KW Phenylalanine hydroxylase; PAH; phha; 4a-carbinolamine dehydratase; PhhB;

KW aromatic amino acid transferase; PhhC; milk protein; casein; PKU;

KW proteinaceous food product; globulin; whey protein; phenylketonuria; PKU;

KW inherited metabolic disorder; impaired brain function; nootropic;

XX cell therapy.

XX OS Escherichia coli.

OS Unidentified.

OS Chimeric.

CC pneumoniae (strain CWL029), and ABL9184-ABL91373 represent DNA encoding pneumoniae. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention. (Updated on 29-Aug-2003 to standardise OS field)

XX SQ Sequence 259 AA;

Query Match Score 1250.5; DB 2;
Best Local Similarity 91.8%; Pred. No. 1.e-117;
Matches 245; Conservative 3; Mismatches 8; Indels 11; Gaps 1;

Db 96 VVSTPFEFNRLWYRLSSRSLWYSYCPFFDQYLEAGLSSDLDHQAVIKKFELTHF 155
4 MVSTPFLTVPSMEKLIS-----KIFLDYLEAFGLLSFLDHQAVIKKFELTHF 52

Qy 156 SYYPPGSFVAPHQYLSSLLQDRYFPIASWYRTLDDNFSLTPDILTHDLLGHVPWLLHPHSFS 215
Db 53 SYYPPGSFVAPHQYLSSLLQDRYFPIASWYRTLDDNFSLTPDILTHDLLGHVPWLLHPHSFS 112
53 SYYPPGSFVAPHQYLSSLLQDRYFPIASWYRTLDDNFSLTPDILTHDLLGHVPWLLHPHSFS 215
Qy 216 EFFINNGRLTKLTVKQVQALPSKKQKORICLQNSLIAITYRCFWTFVESGLLENHEGRKAYG 275
Db 113 EFFINNGRLTKLTVKQVQALPSKKQKORICLQNSLIAITYRCFWTFVESGLLENHEGRKAYG 172
Db 276 AVLISSPOELGHAFIDNVRVPLQIPLDQIIRLPFTNSTPOETLFSIRHFDELVELTSKLEM 335
Db 173 AVLISSSPOELGHAFIDNVRVPLQIPLDQIIRLPFTNSTPOETLFSIRHFDELVELTSKLEM 232
Qy 336 MLDQGILLESIPLYNOKYLSGFEVLCQ 362
Db 233 MLDQGILLESIPLYNOKYLSGFEVLCQ 259

RESULT 3
ID AAE11086 standard; protein; 429 AA.
AC AAE11086
XX ID AAE11086
XX AC AAE11086;
XX DT 18-DEC-2001 (first entry)
XX DE Protein encoded by pFUSAB vector DNA insert sequence.

XX
 FH Location/Qualifiers
 FT .26
 FT /label= Lacz_peptide
 FT Region .27. .28
 FT /label= Linker_peptide
 FT Region .29. .289
 FT /label= phha protein
 FT Region .290. .311
 FT /label= Junction_Peptide
 FT Region .312. .429
 FT /label= phhb protein
 XX PN WO200168822-A2.
 XX PD 20-SEP-2001.
 XX PF 14-MAR-2001; 2001WO-DK000172.
 XX PR 14-MAR-2000; 2000US-00525116.
 XX PA (NILA-) NILAB APS.
 PI Johnson M, Ravn P, Madsen SM, Vrang A, Israelsen H, Bredmose L;
 PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
 XX DR WPI; 2001-590055/66.
 DR N-PSDB; AAD18533.
 XX Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived from a prokaryotic organism, is useful for treating phenylketonuria in mammals.
 PS Example 2; Fig 5; 91pp; English.
 CC The patent discloses novel cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase (PAH) activity such as phenylalanine hydroxylase (phBA), 4a-carbinolamine dehydratase (phB) and aromatic aminotransferase (phBC), which are derived from a prokaryotic organism. The patent also relates to fusion proteins comprising a protein enhancing and/or stabilizing the PAH activity in addition to PAH activity. The cells are useful for producing PAH. The sequences of the invention are also useful for preparing proteinaceous food products (animal protein such as a milk protein derived from casein, globulin or a whey protein) having reduced content of phenylalanine. The method involves contacting the food product starting material with the cells or fusion proteins such that at least part of the phenylalanine content of the starting material is converted into compounds that do not cause phenylketonuria (PKU) by the enzymatically active product. PAH enzyme is useful for manufacturing a medicament for treating PKU, which is an inherited metabolic disorder resulting in an accumulation in the body of L-phenylalanine and metabolites that can cause impaired brain function. The present sequence is a protein encoded by pUS3B vector DNA insert. This sequence comprises a lacz peptide from Escherichia coli, a linker peptide and phB and phA proteins
 XX Sequence 429 AA;
 Query Match 12.5%; Score 237; DB 4; Length 429;
 Best Local Similarity 23.9%; Pred. No. 7e-15;
 Matches 66; Conservative 56; Mismatches 114; Indels 40; Gaps 7;
 Qy 66 SLEPFQNLFWHLISKNQRERGCTDMAVSTPPFNRNLWYRLSSRSLWKSYCPRF 125
 Db 20 SVLEFGPKLKTVQYVARQPD-----DNGTHYPTEHQWNTLITRQKVIEGRACE 72
 Qy 126 FDYDLEAFGLSDFLDHQAVKPFEL-----THSYYPVSFGVAPHQYLSLLDRYFP 179
 Db 73 YLDGIEQIG-----LPHERIPOLDENRVLQATTGVRARVPALIPQTFFELASQQPP 127
 Qy 180 TASVMRTTDKONFSLTDLIRHDLGHWPWLHPSREFINMGRFLFTKVIKEVQALPSKK 239
 Db 128 VATPFRTPFEELDYLQSEPDIFBIFGHCPLINPWFAEFTHTYGLGLKA-----SRE 179

XX
 Qy 240 QRIQITLQSNLIAIVRCWFWTVEGGLIENHEGRKAYGAVLISSPQLGHAFID---NVRVLF 296
 Db 180 ER-----VFLARLYWMWTFEGLVETDGKRIGGGISSLSPKTYSLSDEPHQAFN 231
 Qy 297 PLELDQIIRLPLFNTSPQETLFSTRHDELVELTSK 332
 Db 232 PLE---AMRTPYRIDLQLPLYFVLPLDKRLFQLAQ 264

RESULT 4
 ADD47706 standard; protein; 262 AA.
 XX ID ADD47706
 XX AC ADD47706;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein ITCH, SEQ ID NO 13402.
 XX KW Rat; Pain; neuronal tissue; Gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX KW Rattus norvegicus.
 XX OS WO2003016475-A2.
 XX PN 27-FEB-2003.
 XX PD 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346322P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 PA (PARB) BAYER AG.
 XX PI Woolf C, D'urso D, Beffort K, Costigan M;
 XX DR WPI; 2003-268312/26.
 XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page; 1017pp; English.
 CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the CC polynucleotides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing medicament for treating CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene CC therapy). The sequence presented is a rat protein (shown in Table 2 of CC the specification) which is differentially expressed during pain. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic form directly from WIPO at CC

CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 262 AA;

Query Match Similarity 12.5%; Score 235.5; DB 7; Length 262;

Best Local Similarity 24.5%; Pred. No. 4 .9e-15; Mismatches 52; Indels 33; Gaps 6;

Matches 61; Conservative 52; Mismatches 103; Indels 33; Gaps 6;

Qy 93 DMAVSTPFPENRNIWYRLSSRSRFLSLWKSYCPRFPLDLEAFGLLSDIDQAVIKPFELD 152

Db 13 DNGFPHYPETEHQVANTLITRKVIEGRACQSYLDGIEQLG----LPHERIPOLDEIN 67

Qy 153 -----THFSYYPVSGFVAPHOYQSSLQORYFPIASYMTLQDNFLSPLDLHDLIGHT 206

Db 68 RVLQATIGTRVARYPALIDQPTPEELLASQQFPVATTPBELYDQEPLDFHETFGHC 127

Qy 207 PWLIAHPSPSEFFINGRLFTKVIEKQALPSKKORIQTQSNLIAIVRCFWTVESSLIE 266

Db 128 PLLNPWFELFTTYGKGJKA-----SKEER-----VFLARLYMMTIEFLVNE 171

Qy 267 NHEGRKAYGAVLSSPQELGHAFID--NVRVLPLEPDQQLIRLPENTSTPOETLFSTRHF 323

Db 172 TDQGRRIYEGGILSSPKETVYSSISDEPLHQAFNPLE--AMRTPYRIDLQPLYFVLPDLL 228

Qy 324 DELVELTSK 332

Db 229 KRLFOAQE 237

RESULT 5

ADD48839 Standard; protein; 262 AA.

XX ADD48839; DT 29-JAN-2004 (First entry)

XX Rat Protein 1TOH, SEQ ID NO 14549.

XX Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-PBB-2003.

XX PP 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0344382P.

PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR 2003-268312/26.

XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page: 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC CC that increases or decreases the expression of the polynucleotide sequence

CC CC which is differentially expressed in neuronal tissue of a first animal

CC CC subjected to pain, a method for identifying a compound which regulates

CC CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC CC compounds or their antibodies, the polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 262 AA;

Query Match Similarity 12.5%; Score 235.5; DB 7; Length 262;

Best Local Similarity 24.5%; Pred. No. 4 .9e-15; Mismatches 52; Indels 33; Gaps 6;

Matches 61; Conservative 52; Mismatches 103; Indels 33; Gaps 6;

Qy 93 DMAVSTPFPENRNIWYRLSSRSRFLSLWKSYCPRFPLDLEAFGLLSDIDQAVIKPFELD 152

Db 13 DNGFPHYPETEHQVANTLITRKVIEGRACQSYLDGIEQLG----LPHERIPOLDEIN 67

Qy 153 -----THFSYYPVSGFVAPHOYQSSLQORYFPIASYMTLQDNFLSPLDLHDLIGHT 206

Db 68 RVLQATIGTRVARYPALIDQPTPEELLASQQFPVATTPBELYDQEPLDFHETFGHC 127

Qy 207 PWLIAHPSPSEFFINGRLFTKVIEKQALPSKKORIQTQSNLIAIVRCFWTVESSLIE 266

Db 128 PLLTNWFAWTFQHNTLITRQLKVEGRACQSYLDGIEQLG----VFLARLYWMTEFGLV 171

Qy 267 NHEGRKAYGAVLSSPQELGHAFID--NVRVLPLEPDQQLIRLPENTSTPOETLFSTRH 323

Db 172 TDQGRRIYEGGILSSPKETVYSSISDEPLHQAFNPLE--AMRTPYRIDLQPLYFVLPDLL 228

Qy 324 DELVELTSK 332

Db 229 KRLFOAQE 237

RESULT 6

AAE11161

XX ID AAE11161 standard; protein; 415 AA.

XX AC AAE11161;

XX DT 18-DEC-2001 (First entry)

XX XX phnAB fusion protein fragment.

XX DE Unidentified.

XX KW Phenylalanine hydroxylase; PAH; phnB; 4a-cabindinolamine dehydratase; PhnB;

KW aromatic amino transferase; phnC; milk protein; casein; PKU;

KW proteaceous food product; globulin; whey protein; phenylketonuria; PKU;

KW inherited metabolic disorder; impaired brain function; nootropic;

KW cell therapy; phnAB fusion protein.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Region 21 .46

CC FT Region /note= "PhnAB fusion peptide #1"

CC FT Region 55 .90

CC FT Region /note= "PhnAB fusion peptide #2"

CC FT Region 94 .157

CC FT Region /note= "PhnAB fusion peptide #3"

FT Region	168. .223	Qy	324 DELVLTISK 332
FT Region	/note= "phhab fusion peptide #4"	Db	242 XRLFQIAQE 250
FT Region	228. .272		
FT Region	/note= "phhab fusion peptide #5"		
FT Region	295. .336		
FT Region	/note= "phhab fusion peptide #6"		
FT Region	353. .380		
FT Region	/note= "phhab fusion peptide #7"		
FT Region	396. .415		
FT Region	/note= "phhab fusion peptide #8"		
XX	PN WO200168822-A2.		
XX	PD 20-SEP-2001.		
XX	PP 14-MAR-2001; 2001WO-DK000172.		
XX	PI Arnau J , Jensen SH, Gjetting T, Nielsen E;		
XX	DR 14-MAR-2000; 2000US-00525116.		
XX	PA (NILA-) NILAB APS.		
XX	PT Johnson M, Ravn P, Maddien SM, Vrang A, Israelsen H, Bredmose L;		
XX	PS Example 8; Fig 18; 91PP; English.		
XX	CC Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived from a prokaryotic organism, is useful for treating phenylketonuria in mammals.		
XX	CC The patent discloses novel cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase (PAH) activity such as 4α-carbinolamine dehydratase (phbA), and phenylalanine hydroxylase (phbA), 4α-carbinolamine dehydratase (phbB), and aromatic amino transferase (phbC), which are derived from a prokaryotic organism. The patent also relates to fusion proteins comprising a protein enhancing and/or stabilizing the PAH activity in addition to PAH activity. The cells are useful for producing PAH. The sequences of the invention are also useful for preparing a proteinaceous food product (animal protein such as a milk protein derived from casein, Globulin or a whey protein) having reduced content of phenylalanine. The method involves contacting the food product starting material with the cells or fusion proteins such that at least part of the phenylalanine content of the starting material is converted into compounds that do not cause phenylketonuria (PKU) by the enzymatically active product. PAH enzyme is useful for manufacturing a medicament for treating PKU, which is an inherited metabolic disorder resulting in an accumulation in the body of L-phenylalanine and metabolites that can cause impaired brain function.		
XX	CC The present sequence is phab fusion protein fragment.		
XX	CC Sequence 415 AA;		
Qy	Query Match 12.5%; Score 235.5; DB 4; Length 415;		
Db	Best Local Similarity 24.5%; Pred. No. 9.5e-15; Matches 61; Conservative 52; Mismatches 103; Indels 33; Gaps 6;		
Qy	93 DWA VSTPFFENRNLWYRLLSSRFLSLWYKSCPRFFLDYLEAFGLLSDFLHDQAVIKFFE 152		
Db	26 DNGFIHYBTERHQWNTLITRQLVKIGRACOBYLQIGLQG----LPHERIPQDIE 80		
Qy	153 ----THFSYYPPVSQFWAPHQYLSSLCQDRYPIASWMTLKDNEFSLTPPLIHDQHGV 206		
Db	81 RVLTQATTVRVAVPALIQQTFFELIASQQPVAVATRTPPELDLQQEPPIFEGHIC 140		
Qy	207 PWLHPSSSEFFINMGRILFKTVKRYQALPSKQRIOIQLQSMLIAIVRCMFPTVEGLIE 266		
Db	141 PLLTNPWAETTYKGIGLKA-----SKER----VFLARYMMTIEGLVE 184		
Qy	267 NHEGRKAVGVLSSPQLGHAFID--NVRVLPLELDQITRLPFNTSTPQETLFRIRHF 323		
Db	185 TDQSKRITGGILSSPKRTVYSLSDEPHQAFNPLE--ANRTPYRIDLQQLPYFLVLPDL 241		
Qy	107 WYRLSSRFSLWKS CPCRFLDYLEAFGILLSDFLDH-----QAVIKFFPEDETHFYY 158		
Qy	Sequence 444 AA;		
Qy	Query Match 12.3%; Score 231.5; DB 4; Length 444;		
Db	Best Local Similarity 27.8%; Pred. No. 2.6e-14; Matches 64; Conservative 43; Mismatches 96; Indels 27; Gaps 4;		

RESULT 8

ID ABG96431 Standard; protein: 444 AA.

XX ABG96431

XX DT 11-DEC-2002 (first entry)

XX DE Human ovarian cancer marker OV74.

XX HUMAN; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; non-tuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.

XX OS Homo sapiens.

XX PN WO200271928-A2.

XX PD 19-SEP-2002.

XX PR 14-MAR-2002; 2002WO-US007826.

PR 14-MAR-2001; 2001US-0276025P.

PR 14-MAR-2001; 2001US-027604P.

PR 10-AUG-2001; 2001US-0311132P.

PR 19-SEP-2001; 2001US-0323480P.

PR 26-SEP-2001; 2001US-032457P.

PR 26-SEP-2001; 2001US-0325102P.

PR 26-SEP-2001; 2001US-0325149P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PT Nonahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovaris SG; Meyers RE, Morrissey MP, Olandt Fu, Sen A, Vieby PO, Mills GB; Bast RC, Lu K, Schimadt RE, Zhao X, Glatt K;

XX DR WPI-2002-723277/78.

XX DR N-PSDB; ABS76530.

XX PT Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

XX PS Disclosure: Page 441-442; 48IPP; English.

CC The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing a expression-level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of

Db² 174 WGTYFQELNKLKYPTAACR---EYLNKLPLISKCYGYRBDNIPQLEDVSNLKERTGFSIR 230

Qy 159 PVSGEVVAPROYLSLQDRAFTPIASAVMTIDKDIFSLTDLHLLLGIVPWLHPSFEEF 218

Db 231 PVAGYLSPDPFLSGLAFRPHCTQYVRHSSDPFTPEZDTCHELLGHVPLAEPSPFQES 290

Qy 219 INMGRALFTKVIKEYOALPSKOKRIOQLQSNLIAVRCFWFTYEGLNEHGRKAYGAVL 278

Db 291 QEIG-----LASLGSESEAIVQLAP-----CFTTIEDGLCKQDGQLRVFGAI 334

Qy 279 ISSPOBLGHAFIDNYVRLVPLBQDQIIRLPENTSTPQETLFSRHDELVE 328

Db 335 ISSISELKHALSIGHAKVKPFDPKITCKQBCLITFQDYFVSBSSPEDAKE 384

RESULT 8

ID ABG96431 Standard; protein: 444 AA.

XX AC ABG96431

XX SQ Sequence 444 AA:

Query Match 12.3%; Score 231.5; DB 5; Length 444;

Best Local Similarity 27.8%; Pred. No. 2 6e-14;

Matches 64; Conservative 43; Mismatches 96; Indels 27; Gaps 4;

Qy 107 WYRILSSRFSLWKSICPREFDYLEAFLGGLSDFLDH-----QAVIKFFFELETFSYX 158

Db 174 WGTVFDELNKLKYPTAACR--EYLNKLPLISLQDRAFTPIASAVMTIDKDIFSLTDLHLLLGIVPWLHPSFEEF 230

Qy 159 PVSGEVVAPROYLSLQDRAFTPIASAVMTIDKDIFSLTDLHLLLGIVPWLHPSFEEF 218

Db 231 PVAGYLSPDPFLSGLAFRPHCTQYVRHSSDPFTPEZDTCHELLGHVPLAEPSPFQES 290

Db 219 INMGRALFTKVIKEYOALPSKOKRIOQLQSNLIAVRCFWFTYEGLNEHGRKAYGAVL 278

Db 291 QBIG-----LASLGSESEAIVQLAP-----CYFTTVEFGCKQDGQLRVFGAGL 334

Qy 279 ISSPOBLGHAFIDNYVRLVPLBQDQIIRLPENTSTPQETLFSRHDELVE 328

Db 335 ISSISELKHALSIGHAKVKPFDPKITCKQBCLITFQDYFVSBSSPEDAKE 384

RESULT 9

ID ABG96432 standard; protein: 466 AA.

XX AC ABG96432;

XX DT 11-DEC-2002 (first entry)

XX DE Human ovarian cancer marker OV75.

XX KW Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; Hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; non-tuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.

XX KW Homo sapiens.

XX OS Homo sapiens.

XX PN WO200271928-A2.

XX PD 19-SEP-2002.

XX PR 14-MAR-2002; 2002WO-US007826.

PR 14-MAR-2001; 2001US-0276025P.

PR 14-MAR-2001; 2001US-027604P.

PR 10-AUG-2001; 2001US-0311132P.

PR 19-SEP-2001; 2001US-0323480P.

PR 26-SEP-2001; 2001US-032457P.

PR 26-SEP-2001; 2001US-0325102P.

PR 26-SEP-2001; 2001US-0325149P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PT Nonahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovaris SG; Meyers RE, Morrissey MP, Olandt Fu, Sen A, Vieby PO, Mills GB; Bast RC, Lu K, Schimadt RE, Zhao X, Glatt K;

XX DR WPI-2002-723277/78.

XX DR N-PSDB; ABS76530.

XX PT Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

XX PS Disclosure: Page 441-442; 48IPP; English.

CC The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing a expression-level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of

PR 26-SEP-2001; 2001US-0325102P.
 PR 26-SEP-2001; 2001US-0325149P.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieley PO, Mills GB;
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Giatt K;
 XX
 DR WPI: 2002-723277/78.
 N-PSDB: ABS7631.

XX Disclosure; Page 443-444; 481PP; English.

XX The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. non-tuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the invention.

XX Sequence 466 AA;

Query Match Score 231.5; DB 5; Length 466;
 Best Local Similarity 27.8%; Pred. No. 2.8e-14;
 Matches 64; Conservative 43; Mismatches 96; Indels 27; Gaps 4;

Qy 107 WYRLSSRFSLINKSYCPFFDYLAFGLLSDFLH-----QAVIKFFFELETHESYY 158
 Db 174 WCTVQELNKLTPHTACR---EYLNKLPLSKYCGREDNPOLQEDVSNFLKERTGFSLR 230

Qy 159 FVSGFVAPHQYLSSLLQDYPFPZASVNTLKDNEFLSTPDLLHDLGHPMLHSSFSEFF 218
 Db 231 PVAGYLSPRDFLISGLAARRFHETQYTHSSSPFVTPDPDICELIGHVPLAERSFAQS 290

Qy 219 INNGRLPTKVIEKVOALPSKKRQITLQLQNLIAIVRCWFVTEGSHIBNEGRKAYGATL 278
 Db 291 QEIG-----LASLGASEEAVQKLAT-----CYFFTVEFLCKDQGLRVFGAGL 334

Qy 279 ISSPQELQHAFIDNVYPLPLEDQIIRLPENTSTPOTBLFIRHDELV 328
 Db 335 LSISSELKHALSGHAKVTFD8KITCKQBCLITTFODVYFVSESFDAKE 384

RESUL 10
 ID AAM79208 standard; protein: 444 AA.
 XX

AC AAM79208;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 1870.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PS WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PP 05-FEB-2001; 2001WO-US0001098.
 XX PR 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PR 20-JUN-2000; 2000US-0059075.
 XX PR 19-JUL-2000; 2000US-0062325.
 XX PR 01-SEP-2000; 2000US-0055936.
 XX PR 15-SEP-2000; 2000US-0066561.
 XX PR 20-OCT-2000; 2000US-0069325.
 XX PR 30-NOV-2000; 2000US-00728422.
 XX PA (HYSEQ) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT, Asurdi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZN;
 PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
 XX DR N-PSDB; AAK52341.
 XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 XX PA Claim 20; Page 4255-4256; 6221PP; English.
 XX CC The invention relates to polynucleotides (AAK51456-AAK5345) and the encoded polypeptides (AAM8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and other diseases. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and other diseases.
 CC PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 XX PS Claim 20; Page 4255-4256; 6221PP; English.
 XX CC The invention relates to polynucleotides (AAK51456-AAK5345) and the encoded polypeptides (AAM8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and other diseases. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and other diseases.
 CC PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 XX PS Sequence 444 AA;
 Query Match Score 227.5; DB 4; Length 444;
 Best Local Similarity 27.4%; Pred. No. 6.7e-14;
 Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps 4;
 Qy 107 WYRLSSRFSLINKSYCPFFDYLAFGLLSDFLH-----QAVIKFFFELETHESYY 158
 Db 174 WGTVFQEINKLTPHTACR---EYLNKLPLSKYCGREDNPOLQEDVSNFLKERTGSIR 230
 Qy 159 PVSGFVAPHQYLSSLLQDYPFPZASVNTLKDNEFLSTPDLLHDLGHPMLHSSFSEFF 218
 Db 231 PVAGYLSPRDFLISGLAARRFHETQYTHSSSPFVTPDPDICELIGHVPLAERSFAQS 290
 Qy 219 INNGRLPTKVIEKVOALPSKKRQITLQLQNLIAIVRCWFVTEGSHIBNEGRKAYGATL 278
 Db 335 LSISSELKHALSGHAKVTFD8KITCKQBCLITTFODVYFVSESFDAKE 384
 RESUL 10
 ID AAM79208
 XX

Qy	279 ISSPQELGHAFIDNVRVLPLELDQIIRLFENTSTPOETLFSIRHFDLVE	328	Db	325 LSSISSELKHALSGAKVKPFDKACKOECLLTSFQDQYTFVVSRSFEDAKE	374
Db	335 LSSISSELKHALSGAKVKPFDKACKOECLLTSFQDQYTFVVSRSFEDAKE	384			
			RESULT 11		
AAO17329			AAO17329 standard; protein; 434 AA.		
ID			XX		
XX			XX		
AC			AC		
XX			XX		
DT	08-JUL-2002 (first entry)		DT	29-JAN-2004 (first entry)	
XX			XX		
XX	Neutone specific tryptophane hydroxylase.		DE	Rat Protein P04177, SEQ ID NO 6817.	
XX			XX		
KW	Neuronal tryptophane hydroxylase; nTPH; neuronal disease;		KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; SNI; Chung, chronic constriction injury; CCI; spared nerve injury; SNI; Chung,	
KW	primary haemostasis deficiency; allergy; transplacental; serotonin;		XX		
KW	antiarteriosclerosis; thrombolytic; anticoagulant; immunosuppressive;		OS		
KW	antiallergic; gynaecological.		XX	Rattus norvegicus.	
XX			PN	WO2003016475-A2.	
OS			XX		
Unidentified.			PD	WO2003016475-A2.	
XX			XX	27-FEB-2003.	
PN	WO200217891-A2.		PF	14-AUG-2002; 2002W0-US025765.	
XX			XX		
PD	07-MAR-2002.		PR	14-AUG-2001; 2001US-0312147P.	
XX			PR	01-NOV-2001; 2001US-0344382P.	
PF	27-AUG-2001; 2001NO-DE003178.		PR	26-NOV-2001; 2001US-0333347P.	
XX			XX	(GENO) GEN HOSPITAL CORP.	
PR	31-AUG-2000; 2000DE-01043124.		PA	(FARB) BAYER AG.	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		XX		
XX			PI	Woolf C., D'urose D., Beffort K., Costigan M;	
PI	Walther D., Bader M;		XX		
XX			DR	WPI; 2003-268312/26.	
DR	WPI; 2002-281015/32.		DR	GENBANK; P04177.	
XX			PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.	
XX			XX		
PT			PS	Claim 1; Page; 101 pp; English.	
XX			XX		
XX	Regulating levels of serotonin, useful for diagnosing neuronal disease and treating primary hemostatic deficiency, comprises controlling activity of tryptophan hydroxylase.		CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g., spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g., gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pat/published_pct_sequences.	
XX			XX		
PS	Claim 21; Fig 9; 21pp; German.		CC		
XX			CC		
CC	The present invention relates to a method of influencing the level of serotonin, which involves the specific regulation of TPH (tryptophan hydroxylase) and/or neuron-specific TPH (nTPH) activity. The method is used for the diagnosis of neuronal diseases and for treating deficient primary haemostasis. Also reducing production of serotonin is used to treat arteriosclerosis particularly where associated with diabetes mellitus, and to treat excessive (or normal but unwanted) immune system responses, e.g. allergy, (auto)immune diseases, risks associated with pregnancy, particularly pre-eclampsia, and transplant rejection. The present sequence is a neurone-specific TPH protein		CC		
CC			CC		
PT	Sequence 434 AA;		CC		
XX			CC		
PS	Query Match 107 WYRLISSRFSLWKSQYPRFFLDYLAFFGILSDFLDH-----QAVIKPFELLETHFYY 158	Score 226.5; DB 5; Length 434; Mismatches 43; Indels 27; Gaps 4;	Score 226.5; DB 5; Length 434; Mismatches 43; Indels 27; Gaps 4;		
Qy	164 WGTIFRNLKLYPTHACR--EYLNRLPLLSKYCGREDNPQLVEDSNFLKERTGFSIR 220				
Db	159 PVSGFVAPHOVLISLIQDTRYPLASMTWRLDKDNFLTLPIDHLIGYWLLIPSFSFF 218				
Qy	221 FVAGYLSPRDFLGSGLA弗VRFHCTQVRHSSDPLTYPEPDTCHELGVHLAEPFQS 280				
Db	219 INMGRFLTVKIEVQALPSKRQRIQTLQSNLIAIVRCNFNTVESGLIENHEGRKAYGAVL 278				
Qy	281 QBIG-----LASLGASEBTVQIAT-----CYYFTVERFLCKDGQIRVFQGCL 324				
Db	279 ISSPQELGHAFIDNVRVLPLELDQIIRLFENTSTPOETLFSIRHFDLVE 328				
Qy	Query Match	11.8%; Score 223; DB 7; Length 498;	Query Match	11.8%; Score 223; DB 7; Length 498;	
SQ	Sequence 498 AA;		SQ	Sequence 498 AA;	

Best Local Similarity 26.7%; Pred. No. 2.3e-13; Matches 65; Conservative 39; Nismatches 103; Indels 36; Gaps 5;

CC expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the CC compounds, a method for producing a pharmaceutical composition, a CC polynucleotide, a method for identifying a compound or small molecule that regulates the CC activity in an animal of one or more of the polypeptides given in the CC specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more CC polypeptides or their antibodies. The polynucleotide or the compound that CC modulates its activity is useful for preparing a medicament for treating CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene CC therapy). The sequence presented is a rat protein (shown in Table 2 of CC the specification) which is differentially expressed during pain. Note: CC the sequence data for this patent did not form part of the Printed CC specification, but was obtained in electronic form directly from WIPO at CC ftp://ipo.int/pub/published_pct_sequences.

Qy 156 SYPVSGFVAPHQYLSSLQDRYPIASWMTLKDNTSFSTPDLIHDLIGHTVPWLHPSFS 215
 Db 287 QLRPAGLISARDFLASAFRVRVFOCTQYRHASSPMHSBPDCCHELLOHVPMADRFA 346
 Qy 216 EFFINMGRLFKTVKQVALPSKMKRIOQLTQSNTIAIVRCFWMFTVESGLIENHEGRKAYG 275
 Db 347 QFSQDIGH-----LASLGASDEIEKLST-----VWFWFEGLUKGELKAYG 390
 Qy 276 AVLSSPQEHLGHAFIDNVRVPLDEDQIRILPENTSTPQETLFSIRHF----DELVELTS 331
 Db 391 AGLLSSYGEJLHSLSEPEVRAFDPTAAVQYQDQTYQVVFYSESFNDAKDKRLRNTAS 450

Qy 332 KLE 334
 Db 451 RIQ 453

Query Match 11.8%; Score 223; DB 7; Length 498;
 Best Local Similarity 26.7%; Pred. No. 2.3e-13; Nismatches 103; Indels 36; Gaps 5;

CC Query 11.2 SSRFSLWKS-----YCPRFELDYLEAFLSLSDDLDH-----QAVIKFFEELETHF 155
 CC保守性 65; 匹配数 39; 比较数 103; 缺失数 36; 插入数 5;

Db 227 AEEIAATKEVYVTLKGLYATHACREHLEGGOLLERYCGREDTSIPQLEDSVRFKERTGF 286

Qy 156 SYPPVSGFVAPHQYLSSLQDRYPIASWMTLKDNTSFSTPDLIHDLIGHTVPWLHPSFS 215
 Db 287 QLRPAGLISARDFLASAFRVRVFOCTQYRHASSPMHSBPDCCHELLOHVPMADRFA 346

Qy 216 EFFINMGRLFKTVKQVALPSKMKRIOQLTQSNTIAIVRCFWMFTVESGLIENHEGRKAYG 275
 Db 347 QFSQDIGH-----LASLGASDEIEKLST-----VWFWFEGLUKGELKAYG 390

Qy 276 AVLSSPQEHLGHAFIDNVRVPLDEDQIRILPENTSTPQETLFSIRHF---DELVELTS 331
 Db 391 AGLLSSYGEJLHSLSEPEVRAFDPTAAVQYQDQTYQVVFYSESFNDAKDKRLRNTAS 450

Qy 332 KLE 334
 Db 451 RIQ 453

RESULT 14
 ADE60907 standard; protein; 498 AA.
 ID ADE60907;
 AC ADE60907;
 XX 29-JAN-2004 (First entry)
 DT Rat Protein P04177, SEQ ID NO 6821.
 DB XX
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346342P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 DR 2003-268312/26.
 XX WPI: GENBANK; P04177.
 PR New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 PR Claim 1; Page: 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates CC the expression of a polynucleotide sequence which is differentially

RESULT 14
 AAR50185 standard; protein; 498 AA.
 ID AAR50185;
 AC AAR50185;
 XX 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX Rat tyrosine hydroxylase.

Rat tyrosine hydroxylase.
 XX Human; rat; tyrosine hydroxylase; TH; substitution; N-terminal; KW enhanced enzymatic activity; wild-type; transformation; dopamine; Parkinson's disease; Alzheimer's disease; brain; encapsulation; KW selectively permeable; polymer capsule; antibody.
 XX OS Rattus rattus.
 XX PN USS100436-A.
 XX PD 05-APR-1994.
 XX PP 26-JAN-1993; 93US-00009075.
 XX PR 13-MAR-1991; 91US-00669446.
 XX PA (UNIV) UNIV NEW YORK STATE.
 XX PI Friedhoff AJ, Filer D, Goldstein M, Wu J;

XX WPI; 1994-125849/15.

DR Modified DNA encoding variant tyrosine hydroxylase with an N-terminal PT amino acid substn, and cells contg. it - can be used to treat diseases PT associated with defective function of the enzyme, e.g. Parkinson's PT disease or Alzheimer's disease.

XX Disclosure; Fig 5; 27pp; English.

XX This sequence represents rat tyrosine hydroxylase (TH) and may be used in the production of the variant TH molecules of the invention. These variants contain amino acid substitutions in the N-terminal portion of the molecule, and in the rat molecule these substitutions are present at positions Ser9, Ser19, Ser19, Ser40, Ser40, Glu43 or Arg46. Variants containing one or more of these amino acid substitutions, have substantially enhanced enzymatic activity compared to the wild-type enzyme. The most pref. substitution being Ser40 for Tyr or Leu. DNA encoding the TH variants, and cells transformed with this DNA may be used for treating diseases associated with defective function of TH, or dopamine, e.g. Parkinson's disease and Alzheimer's disease, and effective disorders. The cells can then be implanted into the brain or encapsulated in a selectively permeable polymer capsule which allows release of the cells products but protects them from attack by the hosts antibodies or cells. (Updated on 25-MAR-2003 to correct PCT field.)

XX Sequence 498 AA;

Query Match 11.8%; Score 222; DB 2; Length 498;

Best Local Similarity 26.7%; Pred. No. 2.8E-13; Indels 36; Gaps 5;

Matches 65; Conservative 39; Mismatches 103; Indels 36; Gaps 5;

CC SSRPSLWKS-----YCPRFELDYLEAFGLLSDFLDH-----QAVIKFFPELETHF 155

Qy 112 227 AEEIATKWEYVVTKLKGLYATHACREHLFEGQLLRYCGTREDSTIPOQEDVSRLKEITGF 286

Db 227 QLPRVAGLISAKDPLASLAFLRPFQCTOYRHASSPMHSBEPDCHELLGHVPMЛАДТФА 346

Qy 156 SYPPVSGFVAPHQYLSSLQDRYFPLASVNTLKDMSFTSDPDLTHLGHVPMЛЛHPSFS 215

Db 287 QLPRVAGLISAKDPLASLAFLRPFQCTOYRHASSPMHSBEPDCHELLGHVPMЛАДТФА 346

Qy 216 EFPINNGRFLTKVIEKVQALPSKKKORIQTQSNDLIAIVCFWTFVESGLIENFEGRAYG 275

Db 347 QFSQDG----LASLGASDEEFLKSL-----VWMPTEVEFGICKQNGELKAYG 390

Qy 276 391 AGLISSPQELEGHAFDIDNVRLPLEIDQIRLPEFTSPTQETLFIRHF---DELVELTS 331

Db 391 AGLISSYGEILHSLSLSEPEVRAFDPTAAVQPYODQTIVOPVYFVSESFNDAKDKLRLNYS 450

Qy 332 KLE 334

Db 451 RIQ 453

RESULT 15

AAR36741 standard; protein; 498 AA.

XX AAR36741;

DB 20-SEP-1993 (first entry)

XX Rat tyrosine hydroxylase.

XX Human; rat; tyrosine hydroxylase; substitution; N-terminal; dopamine; neurological disorder; antibody; variant.

XX Rattus ratus.

OS OS

FH Key Location/Qualifiers

FT Modified-site 8

FT /note= "Phosphorylation site"

FT Modified-site 19

FT /note= "Phosphorylation site"

FT

FT Modified-site 40

FT /note= "Phosphorylation site"

FT Modified-site 153

FT /note= "Phosphorylation site"

XX XX

XX PN US5212082A.

XX PD 18-MAY-1993.

XX XX

XX PF 13-MAR-1991; 91US-00669446.

XX PR 13-MAR-1991; 91US-00669446.

XX PA (UNIV) UNIV NEW YORK STATE.

PI Goldstein M, Wu J, Filler D, Friedhoff A;

DR WPI; 1993-175456/21.

XX PT Genetically modified tyrosine hydroxylase having increased activity used for treating neurological disorders e.g. Parkinson's and Alzheimer's diseases and affective disorders.

XX PT Disclosure; Fig 5; 20pp; English.

PS PS

XX CC The sequences given in AAR36740-41 represent the human and rat tyrosine hydroxylase protein respectively. These sequences may be used in the construction of a variant tyrosine hydroxylase which contains at least one amino acid substitution in the N-terminal 55 amino acids. The one amino acid substitution corresponds to an amino acid selected from Ser8, Ser31, Arg37, Arg39, Glu39, Ser40, Ile42, Ile42, Glu43, Asp44, Ala45, Arg46 or Lys47. The enzymatic activity of the variant proteins is at least 3-fold greater than that for the wild type protein. Cells transfected with the CC DNA encoding these proteins may be used for treating neurological CC disorders associated with a deficiency in tyrosine hydroxylase or CC dopamine. These proteins may be used to generate antibodies specific for CC the variant tyrosine hydroxylases to monitor the enzyme during a treatment regimen.

XX SQ Sequence 498 AA;

Query Match 11.7%; Score 221; DB 2; Length 498;

Best Local Similarity 27.4%; Pred. No. 3.6E-13; Indels 36; Gaps 5;

Matches 65; Conservative 37; Mismatches 99; Indels 36; Gaps 5;

Qy 118 WKS-----YCPRFELDYLEAFGLLSDFLDH-----QAVIKFFPELETHSYPPYS 161

Db 233 WKEVYTTLKGJYATHACREHLFEGQLLRYCGTREDSTIPOQEDVSRLKEITGFQLRPVА 292

Qy 162 GFVAPHOYLSLQDRYFPLASVNTLKDMSFTSDPDLTHLGHVPMЛЛHPSFSBFPFINN 221

Db 293 GJLSADDFLASAFRIVFQCTOYRHASSPMHSBEPDCHELLGHVPMЛАДТФАQSQDI 352

Qy 222 GBLFTKVIKEVKQALPSKKKORIQTQSNDLIAIVRCFWTFVESGLIENFEGRAYG 281

Db 353 G-----LASLGASDEEFLKSL-----VWMPTEVEFGICKQNGELKAYGGLSS 396

Qy 282 POEJGHAFIDNVRVLPFLDQIIRLFENTSTPQETLFIRHF---DELVELTSKLE 334

Db 397 YGFLLHSLSSEPEVRAFDPTAAVQPYODQTIVOPVYFVSESFNDAKDKLRLNYS 453

Search completed: March 25, 2004, 14:12:27
Job time : 61 secs

RESULT 3
 i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 i TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 i FILE REFERENCE: 10196-136
 i CURRENT APPLICATION NUMBER: US/09/252,991A
 i CURRENT FILING DATE: 1999-02-18
 i PRIOR FILING DATE: 1998-02-18
 i PRIOR APPLICATION NUMBER: US 60/074,788
 i PRIOR FILING DATE: 1998-07-27
 i NUMBER OF SEQ ID NOS: 33142
 i SEQ ID NO: 29384
 i LENGTH: 308
 i TYPE: PRT
 i ORGANISM: *Pseudomonas aeruginosa*
 i US-09-252,991A-29384

Query Match 11.8%; Score 223; DB 1; Length 498;
 Best Local Similarity 26.7%; Pred. No. 2.e-103; Mismatches 103; Indels 36; Gaps 5;

Query Match 11.2%; Score 223; DB 1; Length 498;
 Best Local Similarity 26.7%; Pred. No. 2.e-103; Mismatches 103; Indels 36; Gaps 5;

Query 11.2 SSRFLWKS-----YCDPFLDLYEARGLLSDFDLH-----QAVIKPFELLETHF 155
 Best Local Similarity 24.6%; Pred. No. 3.2e-17; Mismatches 52; Indels 23; Gaps 5;
 Matches 60; Conservative 52; Mismatches 103; Indels 23; Gaps 5;

Db 227 AEEIAATWKEYVTLLKGLYATHACREHLEFGQULLERYCGYREDSPISQLEDSVRFLKERTGCF 286
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-009-075-5

Query 156 SYYPPSGVAPPHQYLSSRLQDRYFPIASVWRTLDKDFNSLTPLDLHDLGHVPMWILLHPSES 215
 DNGFHYPETPEHQWNTLTLRQLKVEGGACQEYLDDGEQLGLPHDRIPQDDEINRVLQA 118

Db 287 QLRPAGLILLARDPLASLAARRVFOCTQYRHASSPMHSPEPDCCHELLGHVPMALADRTPA 346
 59 DMAYVSTPFFNRNIIWYRJLSSRFSLWKSQPCRPFELDYLFIAFGILLSDFLHD-DAVIKFEL 151

Query 216 EFFFNNGRFLPKVKEVKOQALPSKKKORIOITQIIVRCFWFTVEGSLIENHBGRKAYG 275
 152 ETHEFSYYPVSGEVAPHQYLSSRLQDRYFPIASVWRTLDKDFNSLTPLDLHDLGHVPMWILLH 211

Db 347 QFSQDG-----LASJUGASDEEIEKUST-----VYWFVTFEGLUCKONGELKAYG 390
 Db 119 TTGCRVARPVALIPQFTQFFLILLASQOFPATFIRTPEDYDLOPDIHEIFCHCPLLTN 178

Query 276 AVLSSPQELGHAFIDNVRYVPLPEDIQIIRLPENTSTPQBTLFSIRHF---DELVELTS 331
 212 PSFSEFFINNGRLFKVXKVKQALPSKKKORIOITQIIVRCFWFTVEGSLIENHBGR 271

Db 391 AGLSYYGELHLHSLEPEVRAFDDBTAAVQPYODQTYQPVVFSENFDAOKDLRNAYAS 450
 179 PWFALFHTYTGKLGLKA-----SKER-----VFLARLYMMTIEGLVETQGK 222

Query 332 KLE 334
 272 KAYAVLSSSPQELGHAFID---NVRVPLFIELDQIIRLFENTSTPQETTFSIRHFDELVE 328

Db 451 RIQ 453
 223 RIYGGILSSPKETVYVSLSDPLHQAFNPVLE--AMRTYPRIDLQPLVFLPDLKRLFQ 279

Query 329 LTSK 332
 Db 280 LAQE 283

RESULT 4
 US-08-009-075-4
 Sequence 4, Application US/0809075
 Patent No. 530436
 GENERAL INFORMATION:
 APPLICANT: GOLDSTEIN, Menek
 ATTORNEY/AGENT INFORMATION:
 NAME: TOWNSEND, GUY K.
 REGISTRATION NUMBER: 14,033
 REFERENCE/DOCKET NUMBER: GOLDSTEIN=1A
 TELEPHONE: 202-628-5197
 TELEX/FAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 497 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-009-075-4

Query Match 11.6%; Score 220; DB 1; Length 497;
 Best Local Similarity 26.7%; Pred. No. 5.1e-15; Indels 36; Gaps 5;
 Matches 65; Conservative 38; Mismatches 104; DB 1; Length 497;
 Best Local Similarity 26.7%; Pred. No. 5.1e-15; Indels 36; Gaps 5;
 Matches 65; Conservative 38; Mismatches 104; DB 1; Length 497;

Qy 112 SSRFLSIWKS-----YCPRFEDYLEAFGLISDFLDH-----QAVIKPFELETHF 155
 Db 226 AEEIAWKEVYTTLKGLYATHACGEHLFAPELLRFSGYREDNTIPQLEDSVSRFLKERTGF 285

Qy 156 SYYPVSGFVAPHQYISSLQDRYFPAPSVRTLKDKNFSTPDLIHDLGHVPMILHPSFS 215
 Db 286 QLRPYAGLISARDLASLARVFOCTOYIHRASSEMHSPEPDCCHELLGHVPMLADRTFA 345

Qy 216 EFFINNGRLFPTKVIERKVQLALPSKCRORIQLQSNLNIAITACFWFVTEGSLIENHBRKRAYG 275
 Db 346 QFSQDIG-----LASLGASDEIEEIKLSTLS-----WFVTFEGLKONGEVAYG 389

Qy 276 AVLSSPQEGLHAFIDNVRYLPVLPFLDQIRIPLPFNTSTPOTELFISRHF---DELVEATS 331
 Db 390 AGLSSYGEHLNLCSBEPPEIRAFDPEAAVQPYQDQTYQSVYFVSESESFDARDKLRSYAS 449

Qy 332 KLE 334
 Db 450 RIQ 452

RESULT 5
 US-09-091-117-5
 ; Sequence 5 , Application US/09091117
 ; Patent No. 611589
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Melbourne
 ; TITLE OF INVENTION: Mycoplasma Recombinant Polypeptides and
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: GREENEHOUSE, WINNER and SULLIVAN P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: United States of America
 ; ZIP: 80103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER SYSTEM: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/091,117
 ; FILING DATE: 12 JUNE 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/AU96/000803
 ; FILING DATE: 13-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: AU PN7127
 ; FILING DATE: 13-DEC-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WINNER, Ellen P.
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: +1 303 499 8080
 ; TELEFAX: +1 303 499 8089
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1024 amino acids
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

; ORIGINAL SOURCE:
 ; US-09-091-117-5
 ; Query Match 5.2%; Score 98.5; DB 3; Length 1024;
 ; Best Local Similarity 19.9%; Pred. No. 0.2;
 ; Matches 68; Conservative 41; Mismatches 134; Indels 99; Gaps 11;
 ; Matches 29 ONSQSLORAYSTPYSYRITLQKENKEK---QALARKKCISILEEFFKNLLFVHLLSKN 85
 ; Db 564 QORDSIRNLFSV----IGDLISETNVKNTLHAVKNBELSLVETASTLXIKHL---- 613
 ; Qy 96 OREGCCSTDMAVSTPPFNRLWYRLSSRPSLWKSYCPRREFLDYLEAFGILSDFLDHQAV 145
 ; Db 614 -----NYQKVLVDKBKLNSFKI-----ELLNFEPDPTKDITPT 647
 ; Qy 146 IK--FPELETH-----FSYYPVSFRVAPHQYISSLQDRYFPAPSVMTILDKDNF 192
 ; Db 648 IKKVLFESENVTKLRLCKYENEGFPGTHWAKPIVPEFTAENTFYSAI-----DKT 698
 ; Qy 193 SITELDLTHDLAGHVPMLHPSFSEFTINMGRBLFT-----KVIEKVOALPSKQRQIQT 244
 ; Qy 699 KSIRDLPADML-FGKSLESYNDSDSIIKINGSLTGNLNLNPYHSLITKNGVGYQI 757
 ; Db 245 LOSNLIAIVRCWFTESGLIENHBRKAYGAVLISSPQEG----- 286
 ; Db 758 VVNPNFHIDARLITAELONTVSNPK-----PVKSPVELSLSLFEUVWTIFENSVNQI 810
 ; Qy 287 ----HAFTDNVYRVLPELDQITRLPNTSTPQETLFISRHF 324
 ; Db 811 LRKEYTFKDNLKFEPFKADGSSRLEFDLSKDDQRVPPAFVD 852

RESULT 6
 US-09-198-452A-786
 ; Sequence 786 , Application US/09198452A
 ; Patent No. 559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/03/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 786
 ; LENGTH: 439
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-198-452A-786

Query Match 5.1%; Score 97; DB 4; Length 439;
 Best Local Similarity 22.1%; Pred. No. 0.08; Gaps 19;
 Matches 77; Conservative 51; Mismatches 117; Indels 104; Gaps 19;
 Qy 46 RIIIQKENKEKQDLARHKCISI-L-EFFKNLF--VHLLSKNQREGCSTDMA---- 95
 ; Db 138 RLTHKNPALTHSQVLUHHTVNLKDQVLWQVLFQEOPHLLAVYNTTSKHTSSLVNDKLLA 197
 ; Qy 96 ----VVSTPBFNR----NUWY-RLLSSRSLWWSYCPRFLDYLEA-----FG 134
 ; Db 198 SYTQPISYFSSRVERLBOISLMHQIQYNSLLEIPK---QVFLDQLTAHISGFKQPPFS 253
 ; Qy 135 LLSDFLDQHSAVIFPELETH--FSYYVVS-GEVAPHOYLPSLQDRYPIAS----- 182
 ; Db 254 ILDDL-HHFVDLILYSETHSSESSFFKIAETPNKRHLA---RYKPCAFVTLENMS 306
 ; Qy 183 -VMRTLDKDNF----SLTPDLIHDL-LGHVPWLHPSSEFFINMGRLFTRKVIEYQAL 235
 ; Db 307 WVERLFENLDR FNTLIVDLOEYKONYTP--LSPDSEVF-----ALEKLSS 355
 ; Qy 236 PSKKCQRIQTLQSNLIAIVRCFWFVTEVESLIEHERRKAYGAVLISSPQELGH--AFIDN 292

QY 121 YCPRFP-----L-DLYLEFGILLSDFDHQAVIKPFELTHESTYPSGFVAP 166
 Db 186 YKPLIPEIVSNADTNQDMKKCLTISYRNESLKNNSIR-----NVIMNSAN 236
 QY 167 HOYLSLLQDRYPIASVM-----RTLDKDN-----FSLTPDLTHDLGCHVP 207
 Db 237 DFLQTTTCQFPKLSCIQLNCIDTQFTKLKD-DNTEFDMDPTVQONPLTMHKILQLIL 295
 QY 208 WLIHPS -FSEFFINNMRGLFTKVIEVKQALPSKKKORIOTLOSSNL-LAIVRCFWFVTESG 263
 Db 296 WSIHPSQFDHYSN----QLVALLLL----RINSTDEDLHFQIEDAIWSLVFQ- 343
 QY 264 LIENHESRK-----AYGAV-----LISSP-----OENGHAFD-- 291
 Db 344 LARNFAQQKRVVSYMMPSLYRLLNLLITYGIKVPVYRKLISSGGLYQDSDNDKFVHVQ 403
 QY 292 ---NVRVLPLELDQIRIPFNTSPQETLFISRHDVELVTSKL-----333
 Db 404 LIINLKISPLMKSQYNNVRLNTMEYDKFYELFNFQDVLVEITQKRNRLSNDITNQLS 463
 QY 334 -----BWLMD--QGLLESPIYNQOKYLSGPFEVLC 361
 Db 464 KTPLSIKIMVAEWYLHSICSGISSLSS--NRTVYLLKIFKIFC 502

RESULT 8
 US-08-218-265-12
 ; Sequence 12, Application US/08218265
 ; Patent No. 5925585
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Richard A.
 ; Koleske, Anthony J.
 ; Thompson, Craig M.
 ; APPLICANT: Chao, David M.
 ; TITLE OF INVENTION: No. 5919666el Factors Which Modify Gene
 ; TITLE OF INVENTION: Transcription and Methods of Use Therefor
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militian Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/540,804
 ; FILING DATE: 11-OCT-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/218,265
 ; FILING DATE: 25-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: WHI94-03AA2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1226 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-540-804-12

Query Match 5.0%; Score 95; DB 2; Length 1226;
 Best Local Similarity 18.8%; Pred. No. 0.63; Gaps 25;
 Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps 25;

QY 12 YILKIALKQGSLSLFQNSOSLOAYSTPYYVII-----LOKENKEQALARHKCI 65
 DDB 13 YILE--KLFDMTHYNDSQL-KTWQRQISYFLKLGNCYSRLINNE---1FHMHLY 65
 QY 66 SILEFEKKLFFF-----VHLSSKNOREGCSTDMAVYST-----PFF-----102

Query Match 5.0%; Score 95; DB 2; Length 1226;
 Best Local Similarity 18.8%; Pred. No. 0.63; Gaps 25;
 Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps 25;

QY 66 BFINKMFENFPLPSLHLMWFNDICQDINAPATISSQKEPFVLYTKIDMILHK 125
 DDB 103 -----NRNLWYRLLSSRFSL-----WKS 120
 QY 126 YYVSSSKMSINDENYIINDIKKNNKLNKLXIFQEQSLEVEFPTSNWEI 185

Db 13 YILE---KLIFDMTNHYNDSQL-RTWKROISYFLKLGNCYSLRNLNE---IFHHLVL 65
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1226 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-521-872-12

Qy 66 SILEPERLILF---VHLLSLRNOREGGSTDMAVST-----PFF 102
; Query Match 5.0%; Score 95; DB 3; Length 1226;
; Best Local Similarity 18.8%; Pred. No. 0.63;
; Mismatches 65; Indels 204; Gaps 25;

Db 66 EFINRMENPEFLPLSIHLIMFWNDICQDNTNAVAATITSSQKEPPFLVTKTIDMLLHK 125
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 103 -----NENLYWRLSSRSFL-----WKS 120
; Query Match 5.0%; Score 95; DB 3; Length 1226;
; Best Local Similarity 18.8%; Pred. No. 0.63;
; Mismatches 65; Indels 204; Gaps 25;

Db 126 YYIVSSSKSMINDENYIINIDIKONKNIKLIKLSSLLIKIQBQSLEVEFIPPTSWHE 185
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 121 YCPRF-----LDYLEAFLGILSDFLDHOAVIKPFLETHFSYYVSGFVAP 166
; Query Match 5.0%; Score 95; DB 3; Length 1226;

Db 186 YKPLFEIIVSNADTNQNDSMKKKELISRNESLKNNSSIR-----NVIMSASAN 236
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 167 HOYLSLQDRYFPIASW-----RTLDKN-----FSLTPDLIHDLGHVP 207
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Db 237 DFQLTIVTCRKFQPKLSCIQINCIDTQFTKILD-DNPTEBDWPTVVDQNLTMHKIIQL 295
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 208 WLHPS--FSEFFINGRFLTKVIRKQVALPSKKQRIOQLQSNL-IAIVRCFMFTVBSG 263
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Db 296 WSIHPKRFQDYESEN----OLYAKLIL---RINTTDEDHFQEDAIALSIVFO- 343
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 264 LIENHEGRK-----AGAV-----LISRP---QELGHAFID- 291
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Db 344 LAKNFAAQKVSYMPSPYLRLNLTIGIUKVPTYIIRKLISGGLYQDSNDKPVHVQ 403
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 292 --NVRVLPLDQIIRLPNTSTPQETLFSIRHDELVELTSKL-----333
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Db 404 LLINKISPLMSQINMVLNTMVMEYDVKPEIENFDQLEITEQIKMRILSNDITNLQLS 463
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Qy 334 -----EWMLD---QCLLESTFLPNQEKYVLSGFVLC 361
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

Db 464 KPLSLKIMVAAEWYLISHLCSILSSV---NRTVLKIKIFKFC 502
; Matches 98; Conservative 98; Score 95; DB 3; Length 1226;

RESULT 9
; Sequence 12, Application US/08521872
; Patent No. 6015682
GENERAL INFORMATION:
; APPLICANT: Young, Richard A.
; APPLICANT: Koleske, Anthony J.
; APPLICANT: Thompson, Craig M.
; APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 6015682el Factors Which Modify Gene
TITLE OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,872
FILING DATE: 31-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,265
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

RESULT 10
; Sequence 12, Application US/08590399
; Patent No. 6214588
GENERAL INFORMATION:
; APPLICANT: Young, Richard A.
; APPLICANT: Koleske, Anthony J.
; APPLICANT: Thompson, Craig M.
; APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 6214588el Factors Which Modify Gene
TITLE OF SEQUENCES: 39
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/590,399
 FILING DATE: 26-JUN-1996
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/540,804
 FILING DATE: 11-OCT-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/521,872
 FILING DATE: 31-AUG-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/218,265
 FILING DATE: 25-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: WHI94-03A3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEX/FAX: 617-861-9340
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1226 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-590-399-12

Query Match 5.0% Score 95; DB 3; Length 1226;
 Best Local Similarity 18.8%; Pred. No. 0.63;
 Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps 25;

Query Match 5.0% Score 94; DB 4; Length 1512;
 Best Local Similarity 17.9%; Pred. No. 1.1;
 Matches 64; Conservative 78; Mismatches 117; Indels 78; Gaps 18;

Qy 24 LSLPFONSOISLQRAYSTPSSYRILQKENKEKQALARRHKCISILEFFKNLL-FVHLSL 82
 Db 531 LDILEAEABELLGIDTDINW-VGDEEN-----FANLNNLRKYLHTLKG 574

Qy 24 LQINRBEQLD-----YAPYTINALKRAGQNSNFQPLSUVADFTESEBIFSEQEV 673
 Db 198 LIHDILGHYPWLHPSFSEFFINNGRLP-TKV-----IEKVQALPSKKQRQTQNLI 250

Qy 575 GAMNQ--ATYLGIAHEL-EISYERLJQKLVATSP-----LIDIRL--VQDDDAFR 623

Qy 143 QAVTKPFEELBTHSSYPPVSGFVAPHQYLSLL---QDRYFPIASVMRFLDKDN-FSLTPD 197

Qy 624 LQINRBEQLD-----YAPYTINALKRAGQNSNFQPLSUVADFTESEBIFSEQEV 673
 Db 674 ISEBVIDEFPEVLEPALAELAHHDQVDTAVTLEAPVEVITSVTOENRYTAANEDDIE 733

Qy 12 YIKTKALKURQSLSLFFONSOISLQRAYSTPSSYRIL-----LQENKEKQALARRHKC 65
 Db 13 YILE--KLIFDMTNHYNDSQL-RTWKQISYPLKLGNCYSLRNLKE--IFFHWLY 65

Qy 66 SILEEFFKNLLF---VHJLSSLKQREGCSTDNAVST-----PRF- 102

Db 66 EFINKMNENBFPLPSLHIMIWFNDICQIDNTNAPVAATTSQKEPFLVTKITDMHLK 125

Qy 103 -----NRNLWYRLSSRFSL-----WKS 120

Db 126 YYIVSSSKSMINDENYIINDIKNNKIKNLTLLSILK1FQEQLLEVFLPTSNWEI 185

Qy 121 YCPREF-----LDYLEAFGLSDFLDHQAVIKPELETHPSYXYPVSSFRVAP 166

Db 186 YKPLIFIEIVSNADTNNSMVKCLLEISYNEKNSNSIR-----NYIMSA NAN 236

Qy 167 HQYVSLLQDRYFPASVM-----RTLDKD N-----FSLTPDLIHDLLGHVP 207

Db 237 DFQLTIVTCQFPKPLSCIQLNCDTQFTMLD-DNPTEFDWPTYVDONPLTMHKIQLT 295

Qy 208 WLHHS--FREFFTMGRFLTKVBLQVALPSKQRQIQLQSNL--IAIVRCWFVYESG 263

Db 296 WSIHHSRQFDHYESN----OLVAKLIL---RINSTDELHEFOEDAIWSLYFQ- 343

Qy 264 LIENHEGRK-----AYGAV-----LISSP-----QELGHAFID- 291

Db 344 LAKRNSAQKVSVSTMPMSLYRNLLNITYGIKYKPYTRKLISGLLYQDSNDKFHVQ 403

Qy 292 --NTRVLPLFELDQIIRLPFNTSTPQETLFSIRHDELVELTSKL----- 333

Db 404 LLINRKISPLMKSQYNMVLNVMEYDVKRYEINFNDQLVITEQIRNRLSNDTNLQLS 463

Qy 334 -----EWMLD--QGLIEBIPJPNQEKYLGSGPBVLC 361

Db 464 KTPLSKIKMTAEWYLSHLCGILSSV--NRTVLLKIFKIFC 502

RESULT 11
 US-09-328-352-163
 Sequence 5163; Application US/09328352
 Patent No. 6562958

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328-352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO: 5163
 LENGTH: 1512
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US - 09-328-352-5163

Query Match 5.0% Score 94; DB 4; Length 1512;
 Best Local Similarity 17.9%; Pred. No. 1.1;
 Matches 64; Conservative 78; Mismatches 117; Indels 78; Gaps 18;

Qy 24 LSLPFONSOISLQRAYSTPSSYRILQKENKEKQALARRHKCISILEFFKNLL-FVHLSL 82
 Db 531 LDILEAEABELLGIDTDINW-VGDEEN-----FANLNNLRKYLHTLKG 574

Qy 83 SKNOREGCSTDMAVSTPFFENNLWYRLSSRFSLWYSYCPRFFLDYEAFLGILSDFLDH 142

Db 575 GAMNQ--ATYLGIAHEL-EISYERLJQKLVATSP-----LIDIRL--VQDDDAFR 623

Qy 143 QAVTKPFEELBTHSSYPPVSGFVAPHQYLSLL---QDRYFPIASVMRFLDKDN-FSLTPD 197

Qy 624 LQINRBEQLD-----YAPYTINALKRAGQNSNFQPLSUVADFTESEBIFSEQEV 673

Db 198 LIHDILGHYPWLHPSFSEFFINNGRLP-TKV-----IEKVQALPSKKQRQTQNLI 250

Qy 674 ISEBVIDEFPEVLEPALAELAHHDQVDTAVTLEAPVEVITSVTOENRYTAANEDDIE 733

Qy 251 AIVRCWFVTFESQHLENHEG-----RKAQAVLSSPQEQLGHAFDINVRVPLPEDIQI 303

Db 734 AVBEPFTFBLATELLEMAMESLLKQWFEORTNRSILLQI-QRAMHSLGKGMVGLAEVQA 792

Qy 304 IRLPNNTSTPQETLFSIRH-----DELVELTSLKLEWMHD-----QGLIESI 345

Db 793 IAYQLENAFEQ---FALHHFNSNITYDHLDE-SAIAWLKDADIFHNHYQHFQDGLQQSIL 844

RESULT 12
 US-09-079-030-219
 Sequence 219; Application US/09079030
 Patent No. 6635623

GENERAL INFORMATION:
 APPLICANT: Guevera, Jr., Juan C.
 APPLICANT: Hoogeveen, Ron C.
 APPLICANT: Moore, Paul J.
 TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
 NUMBER OF SEQUENCES: 229
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09-079-030
 FILING DATE: Concurrently Herewith
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: McMillian, Nabeela R.
 REGISTRATION NUMBER: P-43,363

Result No.	Score	Query	Match	Length	DB ID	Description
1	1889	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	10.9	532	10 US-09-963-693-313	Sequence 313, APP
2	1205.5	OM protein - protein search, using sw mode!	10.9	575	15 US-10-369-493-5454	Sequence 5454, APP
3	1206.5	Run on: March 25, 2004, 14:13:29 ; Search time 46 Seconds (without alignments)	10.9	575	15 US-10-369-493-5454	Sequence 5454, APP
4	1206.5	Scoring table: BILOSUM62	10.9	297	14 US-10-369-493-5454	Sequence 5454, APP
5	1206.5	Perfect score: 1889	10.9	404	15 US-10-369-493-5320	Sequence 5320, APP
6	1206.5	Sequence: 1 VHYCRTLDPKYIILAKLQ.....ESTIPLYNQEKYLSGGFELYLCQ 362	10.9	457	15 US-10-369-493-5501	Sequence 5501, APP
7	1206.5	Post-processing: Minimum Match 0%	10.9	2331	15 US-10-353-856-18	Sequence 18, APP
8	1206.5	Total number of hits satisfying chosen parameters: 1065169	10.9	2212	15 US-10-353-856-18	Sequence 18, APP
9	1206.5	Minimum DB seq length: 0	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
10	1206.5	Maximum DB seq length: 20000000000	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
11	1206.5	Post-processing: Maximum Match 100%	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
12	1206.5	Listing first 45 summaries	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
13	1206.5	Database : Published Applications AA,*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
14	1206.5	1: /cggn2_6/podata/1/pubpa/us07_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
15	1206.5	2: /cggn2_6/podata/1/pubpa/us05_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
16	1206.5	3: /cggn2_6/podata/1/pubpa/us06_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
17	1206.5	4: /cggn2_6/podata/1/pubpa/us05_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
18	1206.5	5: /cggn2_6/podata/1/pubpa/us07_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
19	1206.5	6: /cggn2_6/podata/1/pubpa/us08_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
20	1206.5	7: /cggn2_6/podata/1/pubpa/us09_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
21	1206.5	8: /cggn2_6/podata/1/pubpa/us09c_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
22	1206.5	9: /cggn2_6/podata/1/pubpa/us09a_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
23	1206.5	10: /cggn2_6/podata/1/pubpa/us09b_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
24	1206.5	11: /cggn2_6/podata/1/pubpa/us09c_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
25	1206.5	12: /cggn2_6/podata/1/pubpa/us09_new_pub.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
26	1206.5	13: /cggn2_6/podata/1/pubpa/us09b_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
27	1206.5	14: /cggn2_6/podata/1/pubpa/us09c_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
28	1206.5	15: /cggn2_6/podata/1/pubpa/us10b_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
29	1206.5	16: /cggn2_6/podata/1/pubpa/us10c_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
30	1206.5	17: /cggn2_6/podata/1/pubpa/us10_new_pub.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
31	1206.5	18: /cggn2_6/podata/1/pubpa/us10c_pubcomb.pep:*	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
32	1206.5	RESULT 1	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
33	1206.5	US-10-312-273-201	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
34	1206.5	; Sequence 201, Application US/10312273	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
35	1206.5	; Publication No. US2004005567A1	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
36	1206.5	; GENERAL INFORMATION:	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
37	1206.5	; APPLICANT: CHIRON SPA	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
38	1206.5	; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
39	1206.5	; FILE REFERENCE: P25035WO	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
40	1206.5	; CURRENT APPLICATION NUMBER: US/10-3428	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
41	1206.5	; CURRENT FILING DATE: 2002-12-20	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
42	1206.5	; PRIOR APPLICATION NUMBER: 0016353.4	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
43	1206.5	; PRIOR FILING DATE: 2000-07-12	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
44	1206.5	; PRIOR APPLICATION NUMBER: 0017983.8	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
45	1206.5	; PRIOR FILING DATE: 2000-07-21	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
46	1206.5	; PRIOR APPLICATION NUMBER: 0019368.0	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
47	1206.5	; PRIOR FILING DATE: 2000-08-07	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
48	1206.5	; PRIOR APPLICATION NUMBER: 0020440.4	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
49	1206.5	; PRIOR FILING DATE: 2000-08-18	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
50	1206.5	; PRIOR APPLICATION NUMBER: 0022583.9	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
51	1206.5	; PRIOR FILING DATE: 2000-09-14	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
52	1206.5	; PRIOR APPLICATION NUMBER: 0027549.5	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
53	1206.5	; PRIOR FILING DATE: 2000-11-01	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
54	1206.5	; PRIOR APPLICATION NUMBER: 0031706.5	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
55	1206.5	; PRIOR FILING DATE: 2000-12-22	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
56	1206.5	; NUMBER OF SEQ ID NOS: 664	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
57	1206.5	; SOFTWARE: SeqWinn99, version 1.0.02	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
58	1206.5	; SEQ ID NO: 201	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
59	1206.5	; LENGTH: 362	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
60	1206.5	; TYPE: PRT	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
61	1206.5	; ORGANISM: Chlamydia pneumoniae	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
62	1206.5	US-10-312-273-201	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
63	1206.5	Query Match %	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
64	1206.5	Score 1889; DB 15; Length 362;	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
65	1206.5	Best Local Similarity 100.0%; Pred. No. 2.1e-185; Mismatches 0; Indels 0; Gaps 0;	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
66	1206.5	Matches 362; Conservative 0; Matches 362; App	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
67	1206.5	Sequence 313, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
68	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
69	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
70	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
71	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
72	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
73	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
74	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
75	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
76	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
77	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
78	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
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80	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
81	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
82	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
83	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
84	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
85	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
86	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
87	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
88	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
89	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
90	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
91	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
92	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
93	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
94	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
95	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
96	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
97	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
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100	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
101	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
102	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
103	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
104	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
105	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
106	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
107	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
108	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
109	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
110	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
111	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
112	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
113	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
114	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
115	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
116	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
117	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	Sequence 18, APP
118	1206.5	Sequence 5454, APP	10.9	2100.5	15 US-10-353-856-18	

QY¹ 1 VHYCERTIDPKYIKLALKLKRQSLSLFPRNSQSIIQRAYSTPSSYRILQKENKEKOALA 60
Db 1 VHYCERTIDPKYIKLALKLKRQSLSLFPRNSQSIIQRAYSTPSSYRILQKENKEKOALA 60
; Sequence 320, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAM
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIORITY NUMBER: 60/276,025
; PRIORITY NUMBER: 2001-03-14
; PRIORITY NUMBER: 60/325,149
; PRIORITY NUMBER: 60/311,732
; PRIORITY NUMBER: 2001-09-26
; PRIORITY NUMBER: 60/325,102
; PRIORITY NUMBER: 2001-09-26
; PRIORITY NUMBER: 60/324,967
; PRIORITY NUMBER: 2001/09/26
; PRIORITY NUMBER: 60/311,732
; PRIORITY NUMBER: 2001-08-10
; PRIORITY NUMBER: 60/325,102
; PRIORITY NUMBER: 2001-09-19
; PRIORITY NUMBER: 60/323,580
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 320
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-097-340-320

RESULT 3
US-10-097-340-320 ; Sequence 320, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: Griffisis, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments & derivatives thereof and uses thereof, in particular for the diagnosis, prevention & treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 971-003-999
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SEQ ID NO: 1121
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-10-289-162-1121

Query Match 66.2%; Score 1250.5; DB 14; Length 444;
Best Local Similarity 91.8%; Pred. No. 6.1e-120; Mismatches 3; Indels 11; Gaps 1;
Matches 245; Conservative 4;

QY 96 VYSTPFPNRLWYRLLSSRSLWWSYCPRFLDYLEAFOLSPFLDQAVINFELETHF 155
Db 4 MVSTPPTVFMEMKLIS-----KIFLDLEAFOLSPFLDQAVINFELETHF 52
; Query Match 66.2%; Score 1250.5; DB 14; Length 444;
; Best Local Similarity 91.8%; Pred. No. 6.1e-120; Mismatches 3; Indels 11; Gaps 1;
; Matches 245; Conservative 4;

QY 156 SYPVSGPVAHQQLSLQDRYPTIASVNRILDKNESTPDLIHDLLGHFWMLHPSFS 215
Db 53 SYPVSGPVAHQQLSLQDRYPTIASVNRILDKNESTPDLIHDLLGHFWMLHPSFS 112
; Query Match 66.2%; Score 1250.5; DB 14; Length 444;
; Best Local Similarity 91.8%; Pred. No. 6.1e-120; Mismatches 3; Indels 11; Gaps 1;
; Matches 245; Conservative 4;

QY 216 EFPINMGRLFKVIERQALPSKKKRIOTQLOSNLIAIVCPWMTVSCLIEHGRKAYG 275
Db 113 EFPINMGRLFKVIERQALPSKKKRIOTQLOSNLIAIVCPWMTVSCLIEHGRKAYG 172
; Query Match 66.2%; Score 1250.5; DB 14; Length 444;
; Best Local Similarity 91.8%; Pred. No. 6.1e-120; Mismatches 3; Indels 11; Gaps 1;
; Matches 245; Conservative 4;

QY 276 AVLISSQELQHFAIDNVRVPLDEDQIIRLPNTSTPQETLISIRHDVELTSLEW 335
Db 173 AVLISSQELQHFAIDNVRVPLDEDQIIRLPNTSTPQETLISIRHDVELTSLEW 232
; Query Match 66.2%; Score 1250.5; DB 14; Length 444;
; Best Local Similarity 91.8%; Pred. No. 6.1e-120; Mismatches 3; Indels 11; Gaps 1;
; Matches 245; Conservative 4;

QY 336 MLDQGLLESIPLYQEKYLSGEVLCQ 362
Db 233 MLDQGLLESIPLYQEKYLSGEVLCQ 259
; Query Match 66.2%; Score 1250.5; DB 14; Length 444;
; Best Local Similarity 91.8%; Pred. No. 6.1e-120; Mismatches 3; Indels 11; Gaps 1;
; Matches 245; Conservative 4;

RESULT 4
US-10-097-340-322 ; Sequence 322, Application US/10097340
; Publication No. US20030087250A1

GENERAL INFORMATION

APPLICANT: John MONAHAN
 Manjula GANNAVARAM
 Sebastian HOERSCH
 Shubhangi KAMATKAR
 Steve G. KOVATS
 APPLICANT: Rachel E. MEYERS
 APPLICANT: Michael L. MORRISEY
 APPLICANT: Peter OLANDT
 APPLICANT: Ami SEN
 APPLICANT: Peter VEIBY
 Gordon B. MILLS
 Robert C. BAST, Jr.
 APPLICANT: Karen LU
 APPLICANT: Rosemarie SCHMANDT
 Xumei ZHAO

INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer

FILE REFERENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/311,732

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SOFTWARE: PastSeq for Windows Version 4.0

SEQ ID NO: 322

LENGTH: 466

TYPE: PRT

ORGANISM: Homo sapiens

US-10-097-340-322

Query Match Score 231 5; DB 14; Length 466;
 Best Local Similarity 27.8%; Pred. No. 8.6e-15;
 Matches 43; Mismatches 96; Indels 27; Gaps 4;

Qy 107 WYRLISRSRSLWKSICPRFLDYLEAFGLSDELHD-----QAVIKFELETHEFSYY 158
 Db 174 WGTIVFQLNLKLYPHTACR---EYLNKLPLSKYCYREDNIPQLEDVSNFLKERTGFSSR 218

Qy 159 PVSGFVAPQYVLSLQDRYFPIASVTRTLKDKNFSLTPLDLIHLGHYPWLHPSSEBF 218
 Db 231 PVAGYLSPRDFLSGLAFRVPHCTQYVRHSSDPFYPPDTCHELIGHVPLAEFAQS 290

Qy 219 INMGRILFTKVTEKVOALPSKQRIOQTQLOSNLIA1VRCFWTFVEGSLIENHEGRKAYGAVL 278
 Db 281 QEIG----LASIGASEAVQKLAT-----CYFFTVEFLCKQDGOLRVFGAGL 324

Qy 279 ISSPOELGHAFIDNYTVRLVPLDQIIRLPNTSTPOETLFSIRHDELVE 328
 Db 325 LSISISELKHALSIGHAKVPDFPKIACKOECLITSFQDVYFVSESFEDAKE 374

RESULT 6
 US-10-408-456-22

Query Match Score 223; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 4.1e-14;
 Matches 39; Mismatches 103; Indels 36; Gaps 5;

Qy 112 SSRSLWKS-----YCPRFLDYLEAFGLSDELHD-----QAVIKFELETHEFSYY 155
 Db 67 AEEATWKEVYTTLKG1YATHAGEHIEAFALEERFSYREDNIPQLEDVSRLKEETGF 126

Qy 156 SYYPVSGFVAPQYVLSLQDRYFPIASVTRTLKDKNFSLTPLDLIHLGHYPWLHPSSEBF 215
 Db 127 QIRPVAGLISARPLASAFRPFQCTYIRHASSPMSPBECQHMLADTIFA 186

Qy 216 EFFIMGRILFTKVTEKVOALPSKQRIOQTQLOSNLIA1VRCFWTFVEGSLIENHEGRKAYG 275

RESULT 5
 US-10-363-474-1

Sequence 1, Application US/10363474
 Publication No. US200400146521

GENERAL INFORMATION

APPLICANT: WALTHER, Diego
 APPLICANT: BADER, Michael

TITLE OF INVENTION: Method for diagnosing neuronal diseases and for treating primary

Db 187 QFSQDIG-----LASLGASDEEIEKLST-----LYMFTFEGLCKONGEVKAYG 230
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; PRIOR FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 28
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-28

Db 276 AVLISSPQELGHAFIDNYVRLPLEDQIIRLPNTSTPQETLFSIRHF---DELVELTS 331
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; CURRENT APPLICATION NUMBER: US/10/408,456
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; PRIORITY FILING DATE: 2001-10-15
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; PRIORITY FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 26
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-26

Db 291 RIQ 293

RESULT 7

Query Match 11.8%; Score 223; DB 15; Length 501;
 Best Local Similarity 26.7%; Pred. No. 7.2e-14;
 Matches 65; Conservative 39; Mismatches 103; Indels 36; Gaps 5;
 SEQ ID NO: 28

Query Match 11.8%; Score 223; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 4.1e-14;
 Matches 65; Conservative 39; Mismatches 103; Indels 36; Gaps 5;
 SEQ ID NO: 26

RESULT 8
 US-10-408-456-28
 ; Sequence 28, Application US/10408456
 ; Publication No. US/04001368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oxford Biomedica (UK) Limited
 ; APPLICANT: KINGSMAN, et al., Alan John
 ; TITLE OF INVENTION: Vector System
 ; FILE REFERENCE: 674523-2016
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; PRIORITY FILING DATE: 2001-10-15
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; PRIORITY FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Db 112 SSRFLWKS-----YCPRFELDYLEAFGLSLSDFDLH-----QAVIKFFELLETHF 155
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Db 67 AEEIAWKVEYTTLKGLYATHACGEHLFAELLERSGYREDNIPOLQEDVSRLKERTGF 126
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Db 156 SYYPVSGFVAPHOYLSSLQDRYFPLASVMTLDKDFNSLTPDLTHDLCGHVPMILHPPFS 215
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Db 127 QLRPVAGLISARDPLASLA,PRVQFCOTQYRHASSPMHSPEPDCCHELGHVPMILADRTFA 186
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Db 177 QFSQDG-----LASLGASDEEIEKLST-----LYMFVTEFGLKONGEVKAYG 230
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Query Match 11.6%; Score 220; DB 15; Length 338;
 Best Local Similarity 26.7%; Pred. No. 8.3e-14;
 Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps 5;

Db 187 QFSQDG-----LASLGASDEEIEKLST-----LYMFVTEFGLKONGEVKAYG 230
 ; PRIORITY APPLICATION NUMBER: 0024550.6
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY APPLICATION NUMBER: PCT/GB01/04433
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-408-456-24

Qy 276 AVLISSPOELGHAFIDNVRVPLPLEDQIIRLPENTSTPQETLFSIRHPE--DEVELTS 331
 Db 231 AGLISSYCELLCLSEBEEPIRAFDPEAAAVQPYQQDTQYQSIVFVESESERDAKDKLRSYAS 290
 Qy 332 KLE 334
 Db 291 RIQ 293
 :
 :
 RESULT 10
 US-10-154-674-8
 ; Sequence 8, Application US/10154674
 ; Publication No. US2020192694A1
 ; GENERAL INFORMATION
 ; APPLICANT: Yu, Xuanchuan
 ; APPLICANT: Miranda, Maricar
 ; APPLICANT: Hu, Yi
 ; TITLE OF INVENTION: No. US20020192694A1 Human Hydroxylases and Polynucleotides Enc
 ; FILE REFERENCE: IEX-0352-USA
 ; CURRENT APPLICATION NUMBER: US/10/154,674
 ; PRIORITY APPLICATION NUMBER: US-2002-05-23
 ; PRIOR FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 484
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-154-674-8

Query Match 11.5%; Score 216.5; DB 13; Length 484;

Best Local Similarity 26.2%; Pred. No. 3.2e-13; Mismatches 104; Indels 43; Gaps 4;
 Matches 67; Conservative 42; Mismatches 104; Indels 43; Gaps 4;

Qy 117 LWSKSYCPRFEDYLAEFGILSDFLDH-----QAVIKFFELETHFSYYPVSFGFVAPHQ 168
 Db 221 LSKLYPTAACREYLKNPFLITKCYGREDNVQLEDVSMFLERSGFTRPVAGYLSFRD 281

Qy 169 YLSLLQDRYPIASWMTLKDNEFLSTPDLIHDLGHVPNLHPSFSEFFINGRFLTKV 228

Qy 229 TEKVQALPSKKQRIOTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAUILLSPQELGA 288

Db 335 --LASIGASDEDVKLAT-----CYYFFIEFGICKQEGQLRAYAGILLSSIGELKA 384

Qy 289 FIDNVRYVPLPLEDQIIRLPENTSTPQETLFSIRHPE--L 329 -

Db 385 LSDKACVKAFDPKTTCQECLTIFQEAIFYSESPEAKEKMRDFAKSITRPPSVYFNPFY 444

Qy 330 TSKLEMMDQGLLESI 345

Db 445 TQSIELLKDTSTRSTENV 460

RESULT 12
 US-10-154-674-4

; Sequence 4, Application US/10154674
 ; Publication No. US2020192694A1

; GENERAL INFORMATION
 ; APPLICANT: Yu, Xuanchuan
 ; APPLICANT: Miranda, Maricar
 ; APPLICANT: Hu, Yi

; TITLE OF INVENTION: No. US20020192694A1 Human Hydroxylases and Polynucleotides Enc

; FILE REFERENCE: IEX-0352-USA
 ; CURRENT APPLICATION NUMBER: US/10/154,674
 ; PRIOR FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4

Query Match 11.5%; Score 216.5; DB 13; Length 486;

Best Local Similarity 26.2%; Pred. No. 3.2e-13; Mismatches 104; Indels 43; Gaps 4;

Qy 117 LWSKSYCPRFEDYLAEFGILSDFLDH-----QAVIKFFELETHFSYYPVSFGFVAPHQ 168
 Db 223 LSKLYPTAACREYLKNPFLITKCYGREDNVQLEDVSMFLERSGFTRPVAGYLSFRD 282

Qy 169 YLSLLQDRYPIASWMTLKDNEFLSTPDLIHDLGHVPNLHPSFSEFFINGRFLTKV 228

Db 283 FLAGIAYRVPFHCTQYRHGSDFPLTPDPTCHELLGHVPNLHPSFSEFFINGRFLTKV 228

Qy 229 TEKVQALPSKKQRIOTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAUILLSPQELGA 288

Db 337 --LASIGASDEDVKLAT-----CYYFFIEFGICKQEGQLRAYAGILLSSIGELKA 386

Qy 289 FIDNVRYVPLPLEDQIIRLPENTSTPQETLFSIRHPE--L 329 -

Db 387 LSDKACVKAFDPKTTCQECLTIFQEAIFYSESPEAKEKMRDFAKSITRPPSVYFNPFY 446

RESULT 11
 US-10-154-674-6

; Sequence 6, Application US/10154674
 ; Publication No. US2020192694A1

; GENERAL INFORMATION
 ; APPLICANT: Yu, Xuanchuan
 ; APPLICANT: Miranda, Maricar
 ; APPLICANT: Hu, Yi

; TITLE OF INVENTION: No. US20020192694A1 Human Hydroxylases and Polynucleotides Enc

; FILE REFERENCE: IEX-0352-USA
 ; CURRENT APPLICATION NUMBER: US/1/154,674
 ; PRIOR FILING DATE: 2002-05-23
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0

RESULT 13
 US-10-154-674-2
 ; Sequence 2, Application US/10154674
 ; GENERAL INFORMATION:
 ; Publication No. US 20020192694A1
 ; APPLICANT: Yu, Xuanchuan
 ; Miranda, Maricar
 ; APPLICANT: Hu, Yi
 ; TITLE OF INVENTION: Human Hydroxylases and Polynucleotides Encoded by a Human Gene
 ; FILE REFERENCE: LEX-035-2-USA
 ; CURRENT APPLICATION NUMBER: US/10/154,674
 ; CURRENT FILING DATE: 2002-05-23
 ; PRIOR APPLICATION NUMBER: US 60/294,076
 ; PRIOR FILING DATE: 2001-05-29
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 2
 ; LENGTH: 490
 ; TYPE: PRF
 ; ORGANISM: homo sapiens
 ; US-10-154-674-2

Query Match 11.5%; Score 216.5; DB 13; Length 490;
 Best Local Similarity 26.2%; Prod. No. 3.2e-13; Indels 43; Gaps 4;
 Matches 6; Conservative 42; Mismatches 104;

Qy 117 LWKSYCPRFELDYLBAFGILSDFLDH-----QAVIKFFLETHFSYYPVSGFVAPHQ 168
 Db 227 LSCKYPTAACREYKNPFLTKCGYREDNPOLDSMFLKERSGTVRPAGYUSPRD 286
 Qy 169 YLSLQDRYPIASVMRTLDKDNFLSLTDLIHLGLGHVPWLLHPSSEBFINMGRLFKTV 228
 Db 287 FLAGLAYRPHCTOYRIGSDPLYPEPTCHLLGHPYLLDPKFQFSQDQG-----340
 Qy 229 IERYQALPAKKQRQOTLQSNLIAIVRCFWTFITVSGLLENHEGRKAYANVLISSPQEIGHA 288
 Db 341 ---LASLGASDEDYQKLAT-----CYFTTIBGLCQEGOLRAYAGLSSIGELKA 390
 Qy 289 FIDNVRVLPFLDQQLRLENTSPQETFSIHFDELVE-----L 329
 Db 391 LSDKACVKAFKDPKTCQQLITFQAEYVSSREEAKERKMDFAKSITRPFSYVNPY 450
 Qy 330 TSKLEMMLDQGLLESI 345
 Db 451 TQSIBLKDTRSIEN 466

RESULT 14
 US-10-369-493-10768
 ; Sequence 10768, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-1052052 B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; LENGTH: 253
 ; TYPE: PRF

Query Match 10.9%; Score 206.5; DB 15; Length 253;
 Best Local Similarity 26.3%; Prod. No. 1.3e-12; Indels 27; Gaps 4;
 Matches 61; Conservative 36; Mismatches 108;

Qy 106 LWYRLSSRFSLWKSYCPRFELDYLAEFLGLSDFLDHOAVIKFFELB-----THISYYP 159
 Db 9 IWDELYAQMELLPGRACSAFLQGLERID----LGGGVDPFARLSELGALTGNWVVP 63
 Qy 160 VSGFVAPHOYLSDQDRYPIASVMRTLDKDNFLSLTDLIHLGLGHVPWLLHPSSEBFIFI 219
 Db 64 VPMJLIPDHVFWMHLANRFPAGNFIRRETDFYIQEDDVFDVFGHVPMLTDPTYADYMQ 123
 Qy 220 NMGRLFKTVIEKWQALPSKKQRQOTLQSNLIAIVRCFWTFITVSGLLENHEGRKAYAVGLI 279
 Db 124 EYRAGWKAMR-----VNLKAGLALWIVTVERGLVIEDGAPKVYGGIL 168
 Qy 280 SSPQELGHAFI-DNVRVLPFLDQQLRLENTSPQETFSIHFDELVE-----330
 Db 169 SGPREAVFALEGQSPNRMTRDVMRTDYVDDLQPTYFVIESFADLYHQT 220

RESULT 15
 US-09-205-658-313
 ; Sequence 313, Application US/09205658
 ; Patent No. US2001002617A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruvkin, Gary
 ; APPLICANT: Ogg, Scott
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 ; FILE REFERENCE: 0736/251004
 ; CURRENT APPLICATION NUMBER: US/09/205,658
 ; CURRENT FILING DATE: 1998-12-03
 ; EARLIER APPLICATION NUMBER: 08/857,076
 ; EARLIER FILING DATE: 1997-05-15
 ; EARLIER APPLICATION NUMBER: 08/888,534
 ; EARLIER FILING DATE: 1997-07-07
 ; EARLIER APPLICATION NUMBER: US98/10080
 ; EARLIER FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 328
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO: 313
 ; LENGTH: 532
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; US-09-205-658-313

Query Match 10.9%; Score 206.5; DB 9; Length 532;
 Best Local Similarity 25.2%; Prod. No. 3.9e-12; Indels 45; Gaps 8;
 Matches 70; Conservative 47; Mismatches 116;

Qy 104 RNlw-----YRLLSRPSLWKSYCPRFELDYLAEFLGLSDFLD-----QAVIKFFELTHF 155
 Db 251 RKTWG1IYKLR---BLHKHACHQDFNELLERHGCGSENNNPQLEDICKRLKAKTCF 307
 Qy 156 SYYPGVGFVAPHOYLSDQDRYPIASVMRTLDKDNFLSLTDLIHLGLGHVPWLLHPSSE 215
 Db 308 RVRYPZGYSLARDPLAGLAYRVFFCTQYRHADPPYTPBDPTVHLMALFADPDA 367
 Qy 216 EFFINNGRGLFTKVKEVQALPSKKRQIOTLQSNLIAIVRCFWTFITVSGLLENHEGRKAYAVGLI 265
 Db 368 QFSQE-----LASGABEEDIKLATE-----YFSEIEFGUSSDDADSPVK 411
 Qy 266 ---ENHEGRKAYAVGLISSLPOELGHAFIDNVRVLPFLDQIIRLPFTSTPOETLFSIRH 322
 Db 412 ENGSNEFRKVYGAQGILSSAGELOQAVEGSGATIRFDPDVQECLLITFQSAYFYTRN 471
 Qy 323 FDBLVELTSKLEWMLDQGLLESIPLYNQESYLSGPEVL 360
 Db 472 FEEAOQ---KLRMFTNMKRPFIYVN-BYTESYEVL 504

Mon Mar 29 12:10:57 2004

us-09-438-185a-1047.rapb

Page 7

Search completed: March 25, 2004, 14:19:13
Job time : 47 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.
 OM protein - protein search, using sw model
 Run on: March 25, 2004, 14:10:43 ; Search time: 20 Seconds
 (without alignments)
 1741.067 Million cell updates/sec

Title: US-09-438-185A-1047
 Perfect score: 1889
 Sequence: 1 VHYCERTDPLYKILKIALKL.....ESIPLYNQEXYLSSPEVILCQ 362

Scoring table: BLOSUM62
 GapOp 10.0 , Gapext 0.5
 Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR78:
 1: Pir1:
 2: Pir2:
 3: Pir3:
 4: Pir4:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1886	99.8	362	2 E72002	aromatic amino acid aromatic amino acid
2	1886	99.8	362	2 CB6621	phenylalanine-4-hy
3	256.5	13.6	289	2 D82413	phenylalanine-4-hy
4	231.5	12.5	262	2 F83535	tryptophan 5-mono
5	231.5	12.3	444	1 S10489	phenylalanine hydr
6	229.5	12.1	262	2 A53452	tryptophan 5-mono
7	229.5	12.1	444	2 S1199	tyrosine 3-monooxy
8	229.5	12.1	491	2 A28582	tryptophan 5-monoo
9	22.5	12.0	444	1 WHTW	tryptophan 5-monoo
10	226.5	12.0	447	2 A34582	tyrosine 3-monooxy
11	225.5	11.9	498	2 JN0068	tryptophan 5-monoo
12	222.5	11.8	481	2 I51567	tryptophan 5-monoo
13	22.3	11.8	498	1 WHTY	tyrosine 3-monooxy
14	221.5	11.7	491	2 I45983	tyrosine 3-monooxy
15	220	11.6	528	1 WHUY4	tyrosine 3-monooxy
16	219	11.6	579	1 A55369	tyrosine 3-monooxy
17	214	11.3	453	1 WHTF	phenylalanine 4-mo
18	213.5	11.3	452	1 WHUF	phenylalanine 4-mo
19	210.5	11.2	453	2 S15758	phenylalanine 4-mo
20	211.5	11.2	491	2 JL0139	tyrosine 3-monooxy
21	207	11.0	453	2 JQ0766	phenylalanine 4-mo
22	206.5	10.9	575	2 T31509	hypothetical prote
23	197	10.4	453	1 A42271	tryptophan 5-monoo
24	194	10.3	452	2 JC4888	phenylalanine 4-mo
25	189.5	10.0	294	2 C87449	phenylalanine 4-hy
26	178.5	9.4	404	2 T25453	tyrosine 3-monooxy
27	175.5	9.3	457	2 T43194	phenylalanine 4-mo
28	109.5	5.8	1253	2 T45787	disease resistance
29	108.5	5.7	1501	1 B29813	174 K ninaC protein

RESULT 1					
ET2002	aromatic amino acid hyroxylase - Chlamydophila pneumoniae (strain CWL029)	C;Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae	C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000	C;Accession: E72002	R;Kalmi, S.; Mitchell, W.; Marathe, R.; Lammiel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21: 385-389, 1999	A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.	A;Reference number: A72000; MUID:9206606; PMID:10192388	A;Accession: E72002	A;Status: Preliminary	A;Molecule type: DNA
A;Residues: 1-362 <ARN>	A;Cross references: GB:AE001685; GB:AE001363; NID:94377378; PIDN:AAD19183.1; PID:943773	A;Experimental source: strain CWL029	A;Gene: Cpn1046		
Query Match	99.8%	Score 1886 ;	DB 2 ;	Length 362 ;	
Best Local Similarity	99.7%	Pred. No. 2.1e-44 ;			
Matches 361	Conservative 1 ;	Mismatches 0 ;	Indels 0 ;	Gaps 0 ;	
Qy	1 VHYCERTDPLYKILKIALKL.....ESIPLYNQEXYLSSPEVILCQ	Dy	1 MYCYERTDPLYKILKIALKL.....ESIPLYNQEXYLSSPEVILCQ	Dy	1 MYCYERTDPLYKILKIALKL.....ESIPLYNQEXYLSSPEVILCQ
Qy	2 RHKCISILEFFKNLLFYHLLSLSKNQREGCSTDMAVSTPPNRNLYWRLLSRFELWKS	Dy	2 RHKCISILEFFKNLLFYHLLSLSKNQREGCSTDMAVSTPPNRNLYWRLLSRFELWKS	Dy	2 RHKCISILEFFKNLLFYHLLSLSKNQREGCSTDMAVSTPPNRNLYWRLLSRFELWKS
Qy	3 RHCISILEFFKNLLFYHLLSLSKNQREGCSTDMAVSTPPNRNLYWRLLSRFELWKS	Dy	3 RHCISILEFFKNLLFYHLLSLSKNQREGCSTDMAVSTPPNRNLYWRLLSRFELWKS	Dy	3 RHCISILEFFKNLLFYHLLSLSKNQREGCSTDMAVSTPPNRNLYWRLLSRFELWKS
Qy	4 YCRFEDYLEAGFLGLSDFLDQAVKFKELETHFPPVPGFVAHQYLLQDQYFPI	Dy	4 YCRFEDYLEAGFLGLSDFLDQAVKFKELETHFPPVPGFVAHQYLLQDQYFPI	Dy	4 YCRFEDYLEAGFLGLSDFLDQAVKFKELETHFPPVPGFVAHQYLLQDQYFPI
Qy	5 DQITRLPNTSTQETLTSRHDVELTSLKLEMMDQGLESIPINQEQYLSGREVL	Dy	5 DQITRLPNTSTQETLTSRHDVELTSLKLEMMDQGLESIPINQEQYLSGREVL	Dy	5 DQITRLPNTSTQETLTSRHDVELTSLKLEMMDQGLESIPINQEQYLSGREVL
Qy	6 181 ASYMTLDKDNEFLTPD1IHDLIGHTPWLLHPSSEFFINGRFLPKVIEKQALPSKKQ	Dy	6 181 ASYMTLDKDNEFLTPD1IHDLIGHTPWLLHPSSEFFINGRFLPKVIEKQALPSKKQ	Dy	6 181 ASYMTLDKDNEFLTPD1IHDLIGHTPWLLHPSSEFFINGRFLPKVIEKQALPSKKQ
Qy	7 241 RIQTQSNLIAIVRCFWPTVSCLEIIEHGRKAYGAVLSSPOEIGHAFIDNVRLPLEL	Dy	7 241 RIQTQSNLIAIVRCFWPTVSCLEIIEHGRKAYGAVLSSPOEIGHAFIDNVRLPLEL	Dy	7 241 RIQTQSNLIAIVRCFWPTVSCLEIIEHGRKAYGAVLSSPOEIGHAFIDNVRLPLEL
Qy	8 241 RIQTQSNLIAIVRCFWPTVSCLEIIEHGRKAYGAVLSSPOEIGHAFIDNVRLPLEL	Dy	8 241 RIQTQSNLIAIVRCFWPTVSCLEIIEHGRKAYGAVLSSPOEIGHAFIDNVRLPLEL	Dy	8 241 RIQTQSNLIAIVRCFWPTVSCLEIIEHGRKAYGAVLSSPOEIGHAFIDNVRLPLEL
Qy	9 301 DQITRLPNTSTQETLTSRHDVELTSLKLEMMDQGLESIPINQEQYLSGREVL	Dy	9 301 DQITRLPNTSTQETLTSRHDVELTSLKLEMMDQGLESIPINQEQYLSGREVL	Dy	9 301 DQITRLPNTSTQETLTSRHDVELTSLKLEMMDQGLESIPINQEQYLSGREVL
Qy	10 361 CQ 362	Dy	10 361 CQ 362	Dy	10 361 CQ 362

RESULT 2
C86621 aromatic amino acid hydroxylase [Imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: C86621
A;Reference number: A86491; PMID:20330349;
Nucleic Acids Res. 28,
A;Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A;Molecule type: DNA
A;Residues: 1-362 <STO>
A;Cross-references: GB:BA000008; NID:98979419; PIDN:BAA99253_1; GSPPDB:GN00142
A;Experimental source: strain J138
C;Genetics: CPj1046

Query Match Score 99.8%; Best Local Similarity 99.7%; Matches 361; Conservative 0; Indels 0; Gaps 0;

Qy 1 VHYCERTLDPKYLKIALKURQSLISLFFNSQSLORASTPSSYRILQENKEQALA 60
Db 1 MYCERTLDPKYLKIALKURQSLISLFFNSQSLORASTPSSYRILQENKEQALA 60

Qy 61 RHKCISLILEFKNLIVFHLLISLQNRECSSTMAVWTPFFRNLYRLLSSRFIWK 120
Db 61 RHKCISLILEFKNLIVFHLLISLQNRECSSTMAVWTPFFRNLYRLLSSRFIWK 120

Qy 121 YCPRFPLDYLBAFGILSDPFLDHOAVIKPFELETHFSTYPPSGFVAPHOYLSLIQDRYFP 180
Db 121 YCPRFPLDYLBAFGILSDPFLDHOAVIKPFELETHFSTYPPSGFVAPHOYLSLIQDRYFP 180

Qy 181 ASVMTLDKDFNSLTPDLDLHDLGHYPMHLPSSEFFINMGFLFTKVYQALPSKKQ 240
Db 181 ASVMTLDKDFNSLTPDLDLHDLGHYPMHLPSSEFFINMGFLFTKVYQALPSKKQ 240

Qy 241 RIOTQSNLAIIVRCFWFTYESGILHENHGKRAYAVLISSPQGLRAFDINVRVLP 300
Db 241 RIOTQSNLAIIVRCFWFTYESGILHENHGKRAYAVLISSPQGLRAFDINVRVLP 300

Qy 301 DQITLPNTSTPQETLFSRHFDLVELTSKLEWMLDGLLISIPLYNQERYLSGPEV 360
Db 301 DQITLPNTSTPQETLFSRHFDLVELTSKLEWMLDGLLISIPLYNQERYLSGPEV 360

Qy 361 CQ 362
Db 361 CQ 362

RESULT 3
D82413 phenylalanine-4-hydroxylase VCA0828 [Imported] - Vibrio cholerae (strain N16961 serogroup O1; Biotype: El Tor)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82413
R;Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; charlson, D.; Brmoleeva, M.D.; Vanathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; PMID:10952301
A;Status: Preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE004410; NID:99658244; PIDN:AAF96726_1; GSPPDB:GN001
C;Genetics: VCA0828
A;Map position: 2

Query Match Score 256.5%; Best Local Similarity 25.6%; Matches 56; Conservative 56; Indels 25; Gaps 6;
Matches 65; Conservatory 56; Mismatches 108; Del/ins 25;

Qy 106 LWYRLSSRFSLWKSYPREFFDYLEAFLGSSDPLDHQAVI-KFFELTHEFSYYPPVSGFV 164
Db 49 VWHHELTROEVVKTRACOAYLDLNMNLNPDRQLPQEINVLQRETGWQVEPVPA LI 108

Qy 165 APHQYLSSLQDRYPIASUMRTLDKDFNSLTPDLDLGHYPMHLPSSEFFINNGRL 224
Db 109 SFDRFAFLADKKEPVATLRRRREFDTLQEPDFEHETYGHCMALTHDFAAFTVHGQQL 168

Qy 225 PTKVIEKVQALPSKKQRIOTLQSNLIAIVRCFNFVTEQSLIENHEGKRAYAVLISSPQE 284
Db 169 GAKATPKERY-----LARLYNFTVERGLVQEQGOTKLYGGGILSPPGE 212

Qy 285 LGHATIDNV-RVLPDLDQTLRIPNTPQETLFSTIRHDFELVTSK---LEMW-LD 338
Db 213 TLYASESTIPKREFFDQMQLRTYRIDMQPIYYVFDLSOLYQSLQRDMWALWQAMQ 272

RESULT 4
P83535 Phenylalanine-4-hydroxylase PA0872 [Imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: P83535
R;Stover, C.K.; Pham, X.Q.; Erwin, A.I.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho gen
A;Reference number: A82950; PMID:10984043
A;Accession: P83535
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-262 <STO>
A;Cross-references: GB:AE004422; GB:AE004091; NID:99946768; PIDN:AAG04261_1; GSPPDB:GN001

Query Match Score 235.5%; Best Local Similarity 24.5%; Matches 61; Conservatory 52; Mismatches 103; Indels 33; Gaps 6;

Qy 93 DMAVVTTPFFNRNLYWLLSSRFIWKSYCPFRFLDYLEAFGLLSDFLDHQAVIKFPELE 152
Db 13 DNGFPITHYPETEHQVNNTLIRPQLKVEGRACQYLDGIEQLG----LPHERIQLDDEIN 67

Qy 153 -----THFSYPPVSGFVAPHQYLSLQDRYFPIASVMTLDKDFNSLTPDLDHDLGHY 206
Db 68 RVLQATGTGWRVARYVLPFLLPOTFEFLASQQPYPATFIRTPEELDYLQEPDIFHEFGHC 127

Qy 207 PWLLHPSSEFFINNGRLFTKVIKVOALPSKKORITLQSNLIAIVRCFWFTYESGLIE 266
Db 128 PULTNPMFAEFTHTYGLGKIA-----SKEER-----VFLARLYWMTIEFGLV 171

Qy 267 NHEGRKAYAVLISSPQELGHAFID--NTVRLPLEDQIIRLPNTSTPQETLFSIRHF 323
Db 172 TDQGKRITYGGGILSSKETVYSLSDPLHQAFNPLDE--AMRTPYRIDILQPLPFVLPDL 228

Qy 324 DELVETSK 332
Db 229 KRLFQAE 237

RESULT 5

RESULT 8

A;Experimental source: dorsal raphe nucleus
R;Parmon, M.C.; Grima, B.; Cash, C.D.; Maitre, M.; Mallet, J.
PEBS Lett. 206, 43-46, 1986

N;Alternative names: tyrosine 3-hydroxylase
C;Species: Phasianidae gen. sp. (Quail)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 31-Mar-2000

C;Accession: A28582; PH1524

R;Fauquet, M.; Grima, B.; Lamouroux, A.; Mallet, J.

J; Neurochem. 50, 142-148, 1988

A;Title: Cloning of quail tyrosine hydroxylase: amino acid homology with other hydroxylases
A;Reference number: A28582; MUID: 88089590; PMID: 2447231

A;Molecule type: mRNA
A;Residues: 1-491 <PFA>
A;Cross-references: GB:M24778; NID:9213649; PIDN:AAA49514.1; PMID:9213650

R;Fauquet, M.; Boni, C.

J; Neurochem. 60, 274-281, 1993

A;Title: The quail tyrosine hydroxylase gene promoter contains an active cyclic AMP-response element
A;Reference number: PH1524; MUID:93107922; PMID:8093261

A;Molecule type: DNA
A;Residues: 1-30 <FA2>

C;Superfamily: bioperin: catecholamine biosynthesis; iron; metalloprotein; oxidoreductase; F,324,329,369/Binding site: iron (His, His, Glu) #status predicted

Query Match Score 229.5; DB 2; Length 491;
Best Local Similarity 29.1%; Pred. No. 9.7e-11;
Matches 66; Conservative 34; Mismatches 100; Indels 27; Gaps 4;

Qy 107 WYRLSSRPSLWYSYCPRFLDYLEAFGLSLSPFLDH-----QAVIKPFPELETHFSYY 158
Db 226 WKEYSTKSLYTHACK--EYLEAFNLLEKFGYNNNTPQLEEVSRLKERTGFOLL 282

Qy 159 PVSGFVAPHOYLSSLQDRYFPIASVMRTLDKDNFLSLTPDILHDLGHVPWLHPSFSEF 218
Db 283 PVRGILSAAFDLASLAFVFOCTOYIRHASSPMHSBPCDCCBLLGHVPLADKTAQFS 342

Qy 219 INMGRLFTKVIEYQALSKKQRIOQTLSNLIAIVRCFWTVEGLIENHEGRKAYAVI 278
Db 343 QDIG-----LASIGATDEIEKLATL-----YWFTVEGLCRONGVKAYAGL 386

Qy 279 ISSPOELGHAFIDNVRVLPFLDQIIRLPNTSTPQETLFSIRHFDLVE 328
Db 387 LSSTGELTHSLSDPEVNDFDPAAAV&PCQDQPYOPRYFVSESESFEDAKE 384

RESULT 10

A;Experimental source: pineal gland
R;Parmon, M.C.; Grima, B.; Carver, C.H.; Joh, T.H.; Park, D.H.

J; Neurochem. 51, 312-316, 1988

A;Title: Sequence of two mRNAs encoding active rat tryptophan hydroxylase
A;Reference number: JL0034; MUID: 88244702; PMID:3379411

A;Accession: JL0034

A;Molecule type: mRNA
A;Residues: 1-444 <DBA>

A;Cross-references: GB:X53501; NID:957760; PIDN:CAA37579.1; PID:957761

R;Kim, K.S.; Wessel, T.C.; Stone, D.M.; Carver, C.H.; Joh, T.H.; Park, D.H.

Brain Res. Mol. Brain Res. 9, 277-283, 1991

A;Title: Molecular cloning and characterization of cDNA encoding tryptophan hydroxylase
A;Reference number: A60034; MUID:91245924; PMID:1645130

A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-444 <KIM>

N;Alternative names: tryptophan 5-monooxygenase (EC 1.14.16.4) - rat
C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Mar-2000

C;Accession: JL0034; A60034; A24467

R;Parmon, M.C.; Guibert, B.; Levrat, V.; Ehret, M.; Maitre, M.; Mallet, J.

A;Title: Sequence of two mRNAs encoding active rat tryptophan hydroxylase
A;Reference number: JL0034; MUID: 88244702; PMID:3379411

A;Accession: JL0034

A;Molecule type: mRNA
A;Residues: 1-444 <DBA>

A;Cross-references: GB:X53501; NID:957760; PIDN:CAA37579.1; PID:957761

R;Kim, K.S.; Wessel, T.C.; Stone, D.M.; Carver, C.H.; Joh, T.H.; Park, D.H.

Brain Res. Mol. Brain Res. 9, 277-283, 1991

A;Title: Molecular cloning and characterization of cDNA encoding tryptophan hydroxylase
A;Reference number: A60034; MUID:91245924; PMID:1645130

A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-444 <KIM>

RESULT 9

WHRTW
tryptophan 5-monooxygenase (EC 1.14.16.4) - rat

N;Alternative names: tryptophan 5-monooxygenase
C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Mar-2000

C;Accession: JL0034; A60034; A24467

R;Parmon, M.C.; Guibert, B.; Levrat, V.; Ehret, M.; Maitre, M.; Mallet, J.

A;Title: Sequence of two mRNAs encoding active rat tryptophan hydroxylase
A;Reference number: JL0034; MUID: 88244702; PMID:3379411

A;Accession: JL0034

A;Molecule type: mRNA
A;Residues: 1-444 <DBA>

A;Cross-references: GB:X53501; NID:957760; PIDN:CAA37579.1; PID:957761

R;Kim, K.S.; Wessel, T.C.; Stone, D.M.; Carver, C.H.; Joh, T.H.; Park, D.H.

Brain Res. Mol. Brain Res. 9, 277-283, 1991

A;Title: Molecular cloning and characterization of cDNA encoding tryptophan hydroxylase
A;Reference number: A60034; MUID:91245924; PMID:1645130

A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-444 <KIM>

RESULT 11

WYRLSSRPSLWYSYCPRFLDYLEAFGLSLSPFLDH-----QAVIKPFPELETHFSYY 158
Best Local Similarity 27.4%; Pred. No. 1.5e-10;
Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps 4;

Qy 107 WYRLSSRPSLWYSYCPRFLDYLEAFGLSLSPFLDH-----QAVIKPFPELETHFSYY 158
Db 177 WGTIFRELNKLYTHACR--EYLRNPLLSKVCYGYREDNVQLEDNSNFKERTGGSIR 230

Qy 159 PVSGFVAPHOYLSSLQDRYFPIASVMRTLDKDNFLSLTPDILHDLGHVPWLHPSFSEFF 218
Db 231 PVAGYLSPRDFLSLAFLFRHTQVYHSSDPLYTPBDTCHELLGVPLLAEPSPFQFS 290

Qy 219 INMGRLFTKVIEYQALSKKQRIOQTLSNLIAIVRCFWTVEGLIENHEGRKAYAVI 278
Db 291 QEIG-----LASLGASEBEVYQKAT-----QEFVTFEGLOCKDGDLVRFAGL 334

Qy 279 ISSPOELGHAFIDNVRVLPFLDQIIRLPNTSTPQETLFSIRHFDLVE 328
Db 335 ISSISSELHALSGHAKVKBPFDPKVACQECLITSFQDVYFVSESESFEAKE 384

RESULT 12

A;Experimental source: pineal gland
R;Parmon, M.C.; Grima, B.; Carver, C.H.; Joh, T.H.; Park, D.H.

J; Neurochem. 5, 88-96, 1990

A;Title: Characterization and chromosomal mapping of a cDNA encoding tryptophan hydroxylase
A;Reference number: A34582; MUID:90243261; PMID:90243261

A;Accession: A34582

A;Status: Preliminary

A;Molecule type: mRNA
A;Residue: 1-447 <STO>

A;Species: Mus musculus (house mouse)

C;Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 31-Mar-2000

C;Accession: A34582

R;Stoll, J.; Kozak, C.A.; Goldman, D.

Genomics 7, 88-96, 1990

A;Title: Characterization and chromosomal mapping of a cDNA encoding tryptophan hydroxylase
A;Reference number: A34582; MUID:90243261; PMID:90243261

A;Accession: A34582

A;Status: Preliminary

A;Molecule type: mRNA
A;Residue: 1-447 <STO>

A;Cross-references: GB:J04758; NID:9202113; PIDN:AAA63401.1; PID:9202114

A;Note: The authors translated the codon AAC for residue 405 as Gln

C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: bioperin; iron; metalloprotein; oxidoreductase; phosphoprotein

F,275,280,320/Binding site: iron (His, His, Glu) #status predicted

Query Match Score 226.5; DB 2; Length 447;
Best Local Similarity 27.4%; Pred. No. 1.5e-10;
Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps 4;

Qy 107 WYRLSSRPSLWYSYCPRFLDYLEAFGLSLSPFLDH-----QAVIKPFPELETHFSYY 158
Db 177 WGTIFRELNKLYTHACR--EYLRNPLLSKVCYGYREDNVQLEDNSNFKERTGGSIR 230

Qy 159 PVSGFVAPHOYLSSLQDRYFPIASVMRTLDKDNFLSLTPDILHDLGHVPWLHPSFSEFF 218
Db 234 PVAGYLSPRDFLSLAFLFRHTQVYHSSDPLYTPBDTCHELLGVPLLAEPSPFQFS 293

Qy 219 INMGRLFTKVIEYQALSKKQRIOQTLSNLIAIVRCFWTVEGLIENHEGRKAYAVI 278

Db 294 QEIG-----LASLGASEETVQKLAT-----CYFTVERGLCKRGDGLRVEGAGL 337
 C;Cross-references: GB:L20679; NID:9450644; PID:AAA21306_1; PID:9450645
 C;Superfamily: Phenylalanine 4-monoxygenase
 C;Keywords: biotin; iron; metalloprotein; oxidoreductase
 P;Xref:354/Binding site: iron (His, His, Glu) #status predicted

Query Match 11.9%; Score 223.5; DB 2; Length 496;
 Best Local Similarity 29.5%; Pred. No. 2.9e-10;
 Matches 70; Conservative 38; Mismatches 90; Indels 39; Gaps 9;

Db 107 WYRLSSRFSLMKSYCPFFDYLEAFGLSDFLDH----QAVIKFFLETHFSYY 158
 Db 211 WGTIVFRLKLYATHACR---EYKLNLPLSKHCGYREDNIPQLEVSFRERCTFIR 267
 Query Match 11.8%; Score 223.5; DB 2; Length 481;
 Best Local Similarity 29.5%; Pred. No. 2.9e-10;
 Matches 70; Conservative 38; Mismatches 90; Indels 39; Gaps 9;

Db 159 PVSGFVAPHOYLSSLQDRYFPPIASWRTLDKDNFLTDPLIHDGLHVPMLHPSSEF 217
 Db 268 PYAGLSPRDLFLAGLFRVFTQYRH-DSDPPLNTPEPDTCHELLGHVPILAEPFAQF 326
 Query Match 11.8%; Score 223.5; DB 2; Length 481;
 Best Local Similarity 29.5%; Pred. No. 2.9e-10;
 Matches 70; Conservative 38; Mismatches 90; Indels 39; Gaps 9;

Db 218 INMGRILFTKVIEKQVQLPSKQRICTLQSNLIAIVRCFWPTVSESSLIEHGRKAYGAV 277
 Db 327 SQBIG-----LASLGASDEAVQKLAT-----CYFTVEFLICKQEGKLKYGAG 370
 Db 371 LISSISELKHSLSGNAKVKWPFD-----PMVTCN-QECI--ITSSQELYFVSESEB 417

RESULT 13

Db 278 LSSPQEIGHAFTDNTRVLPFLDQIIRLPPNTSTQETIFSRHDELVELTSKIE 334
 Db 371 LISSISELKHSLSGNAKVKWPFD-----PMVTCN-QECI--ITSSQELYFVSESEB 417

Db 107 WYRLSSRFSLMKSYCPFFDYLEAFGLSDFLDH----QAVIKFFLETHFSYY 158
 Db 233 WKEVYATKLYATHACR---EHLAEFOLLEYRCGYREDNIPQLEDSFLKERTGFQLR 289
 Query Match 11.9%; Score 223.5; DB 2; Length 496;
 Best Local Similarity 27.5%; Pred. No. 2.1e-10; Gaps 5;
 Matches 66; Conservative 42; Mismatches 101; Indels 31; Gaps 5;

Db 159 PVSGFVAPHOYLSSLQDRYFPPIASWRTLDKDNFLTDPLIHDGLHVPMLHPSSEF 218
 Db 290 PYAGLSPRDLFLAGLFRVFTQYRH-DSDPPLNTPEPDTCHELLGHVPILAEPFAQF 349
 Query Match 11.9%; Score 223.5; DB 2; Length 496;
 Best Local Similarity 29.5%; Pred. No. 2.9e-10;
 Matches 70; Conservative 38; Mismatches 90; Indels 39; Gaps 9;

Db 218 INMGRILFTKVIEKQVQLPSKQRICTLQSNLIAIVRCFWPTVSESSLIEHGRKAYGAV 278
 Db 350 QDIG-----LASLGASDEAVQKLAT-----VWVFVVEFLCKONGELKAYAGL 393
 Query Match 11.9%; Score 223.5; DB 2; Length 496;
 Best Local Similarity 29.5%; Pred. No. 2.9e-10;
 Matches 70; Conservative 38; Mismatches 90; Indels 39; Gaps 9;

Db 394 LSSYGEULLHSLSBEPETRAFDPTAAVQPYQQTIVFVSEFSDAKDQLRNYSR1.Q 453
 Db 395 QDIG-----LASLGASDEAVQKLAT-----VWVFVVEFLCKONGELKAYAGL 393
 Db 396 LSSYGEULLHSLSBEPETRAFDPTAAVQPYQQTIVFVSEFSDAKDQLRNYSR1.Q 453
 Query Match 11.9%; Score 223.5; DB 2; Length 496;
 Best Local Similarity 29.5%; Pred. No. 2.9e-10;
 Matches 70; Conservative 38; Mismatches 90; Indels 39; Gaps 9;

RESULT 14

Db 151567 tryptophan 5-monoxygenase (EC 1.14.16.4) - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 31-Mar-2000

Db 151567 tryptophan 5-monoxygenase (EC 1.14.16.4) - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Accession: X04914; NID:957355; PID:CAA2884_1; PID:957336
 C;Function: catalyzes the 3'-hydroxylation of tyrosine to 3',4'-dihydroxyphenylalanine
 C;Description: catalyzes the 3'-hydroxylation of tyrosine to 3',4'-dihydroxyphenylalanine
 C;Pathway: catecholamine biosynthesis
 A;Note: this is the rate-limiting step in catecholamine biosynthesis
 C;Superfamily: phenylalanne 4-monoxygenase
 C;Keywords: biotin; iron; metalloprotein; monoxygenase
 F;8/Binding site: phosphate (Ser) (covalent) (by unidentified kinase) #status experimental
 F;8/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status experimental
 A;Residues: 1-481 <GRE>

Query Match 11.8%; Score 223; DB 1; Length 498;
Best Local Similarity 26.7%; Pred. No. 3..3e-10;
Matches 65; Conservative 39; Mismatches 103; Indels 5;

Qy 112 SSRPSLWKS-----YCPRFELDYEAFGLISDFLDH-----QAVIKFFELETHF 155
Db 227 AEEATWKEVVTIQLKGLYATHACREHJEGFQLLERYGYREDIPIQEDVRFKERTGF 286
Qy 156 SYPVSGFVAPHQYLISLQLDRYRPIASVMRTLDKDNEISLTPLDLHGHYPWLHPSFS 215
Db 287 QLRVAGLILSARDTLASLAFRVQCTOYRHASSPMHSPEPDCHELLGHVPLMLADRTFA 346

Qy 216 EFTINMGRIFTYKEVKQALPSKKQRITQIQLQSNLIAIVRCMFPTVESGLIENHEGRKAYG 275
Db 347 QPSDIDG-----LASLGVSDEEIKLST-----VWMTFTVERGLCKQNGELKAYG 390

Qy 276 AVLISSPQLGHAFIDNRYVRLPLEDQIIRLPNTSTPQETLFISRHF---DELVELTS 331
Db 391 AGLISSYGGELLHSLSSEEPVRAFPDPDTAAVQPYQDQTYQPVYVFVSESFSNDAKDYLENYAS 450

Qy 332 KLE 334
Db 451 RIQ 453

RESULT 14

I45983 tyrosine 3-monoxygenase (EC 1.14.16.2) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C;Accession: I45983
R;D.Mello, S.R.; Weisberg, R.P.; Stachowiak, M.K.; Turzai, L.M.; Gioio, A.B.; Kaplan, B.J.; Neurosci. Res. 19, 440-449, 1988
A;Title: Isolation and nucleotide sequence of a cDNA clone encoding bovine adrenal tyrosine 3-monoxygenase
A;Reference number: I45983; MUID:88255287; PMID:289537
A;Accession: I45983
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-491 <DXM>
A;Cross-references: GB:W346794; PID:AAA30773.1; PID:g163751
C;Superfamily: Phenylalanine 4-monoxygenase
C;Keywords: biotin; iron; metalloprotein; monooxygenase; oxidoreductase
F; 329,329,369/Binding site: iron (His, Glu) #status predicted

Query Match 11.7%; Score 221.5; DB 2; Length 491;
Best Local Similarity 27.1%; Pred. No. 4..3e-10;
Matches 65; Conservative 42; Mismatches 102; Indels 31; Gaps 5;

Qy 107 WYRLSSPFISWKSICPPLDYEAFGLISDFLDH-----QAVIKFFELETHFSYY 158
Db 226 WKEVISTLGRGYPHTACR--EHLEFAEFLERFCCYREDIPIQEDVRFKERTGFQLR 282

Qy 159 PVSFGFVAPHQYLISLQLDRYRPIASVMRTLDKDNEISLTPLDLHGHYPWLHPSFSBF 218
Db 283 PAAGLILSARDTLASLAFRVQCTOYRHASSPMHSPEPDCHELLGHVPLMLADRTFA 342

Qy 219 INMRGLPTKVIEVKQALPSKKQRITQIQLQSNLIAIVRCMFPTVESGLIENHEGRKAYGAVL 278
Db 343 QDIG-----LASLGVSDEEIKLST-----LYNFTVERGLCKQNGELKAYGAGL 386

Qy 279 ISSPQLGHAFIDNRYVRLPLEDQIIRLPNTSTPQETLFISRHF---DELVELTSKUE 334
Db 387 ISSYGGELLHSLSSEEPVRAFPDPDTAAVQPYQDQTYQPVYVFVSESFSNDAKDYLENYASRQQ 446

RESULT 15

WHUY4 tyrosine 3-monoxygenase (EC 1.14.16.2), splice form 4 - human
N;Alternate names: Tyrosine 3-hydroxylase
N;Contains: tyrosine 3-monoxygenase, splice form 1; tyrosine 3-monoxygenase, splice fo

C;Species: Homo sapiens (man)
C;Date: 31-Mar-1999 #sequence_revision 31-Mar-1989 #text_change 16-Jun-2000
C;Accession: A30022; A62625; A62021; JE0012; JE0014; A27791; C27791; PN
R;Negatsu, T.; submitted to GenBank, December 1987
A;Accession number: A94509
A;Molecule type: mRNA
A;Residues: 1-528 <NGAG1>
A;Cross-references: GB:W17589; NID:9339680; PID:AAA61179.1; PID:g339681
R;Kaneda, N.; Kobayashi, K.; Ichinose, H.; Kishi, F.; Nakazawa, A.; Kurosoawa, Y.; Fujita, R.; Le Bourdelle, B.; Boni, C.; Horellou, P.; Dumas, S.; Grima, B.; Mallet, J.; Neurochem. 50, 98-991, 1987
A;Title: Isolation of a novel cDNA clone for human tyrosine hydroxylase: alternative RNA
A;Reference number: A90136; MUID:28878614; PMID:2887169
A;Accession: A26825
A;Molecule type: mRNA
A;Residues: 1-94 <NGAG2>
A;Cross-references: GB:W17589; NID:9339680; PID:g339681
R;Kobayashi, K.; Kaneda, N.; Ichinose, H.; Kishi, F.; Nakazawa, A.; Kurosoawa, Y.; Fujita, R.; Horellou, P.; Dumas, S.; Grima, B.; Mallet, J.; Neurochem. 50, 98-991, 1987
A;Title: Analysis of the 5' region of the human tyrosine hydroxylase gene: combinatorial
A;Reference number: A60201; MUID:88117543; PMID:2892893
A;Accession: A60201
A;Molecule type: mRNA
A;Residues: 1-65 <LEB>
A;Cross-references: GB:M24790; NID:g556223; PID:AAA61174.1; PID:g556224
A;Title: Structure of the human tyrosine hydroxylase gene: alternative splicing from exon 1
A;Reference number: JE0012; MUID:89008200; PMID:2902075
A;Accession: A60201
A;Molecule type: DNA
A;Residues: 1-30,62-135 <KOBJ1>
A;Cross-references: GB:DO0261; NID:9220099; PID:BA25094.1; PID:g3951764
A;Experimental source: splice form 1
A;Note: this splice form is produced by an alternative donor site within exon 1
A;Accession: JE0013
A;Molecule type: DNA
A;Residues: 1-14,62-135 <KOBJ2>
A;Experimental source: GB:DO0261; NID:9220099; PID:BA25097.1; PID:g2951767
A;Accession: JE0012
A;Molecule type: DNA
A;Residues: 1-30,62-135 <KOBJ3>
A;Cross-references: GB:DO0261; NID:9220099; PID:BA25095.1; PID:g3951765
A;Experimental source: splice form 3
A;Note: this splice form is produced by an alternative donor site within exon 1
A;Accession: JE0013
A;Molecule type: DNA
A;Residues: 1-36,62-135 <KOBJ4>
A;Experimental source: splice form 3
A;Accession: JE0014
A;Molecule type: DNA
A;Residues: 1-35,62-135 <KOBJ5>
A;Cross-references: GB:DO0261; NID:9220099; PID:BA25095.1; PID:g3951765
A;Experimental source: splice form 3
A;Note: this splice form is produced by an alternative donor site within exon 1
A;Accession: JE0013
A;Molecule type: mRNA
A;Residues: 1-34,62-135 <GR1>
A;Cross-references: GB:X05290; NID:g32501; PID:CA28908.1; PID:g32502
A;Experimental source: splice form 1
A;Note: this isozyme is produced by use of an alternative donor site within exon 1
A;Accession: C27791
A;Molecule type: mRNA
A;Residues: 30-35-528 <GR13>
A;Cross-references: GB:X05290; NID:g32501
A;Experimental source: splice form 3
A;Accession: C27791
A;Molecule type: mRNA
A;Residues: 1-34,62-528 <GR12>
A;Cross-references: GB:X05290; NID:g32501
A;Note: this isozyme is produced by use of an alternative donor site within exon 1
R;Ichirose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans
A;Reference number: PN0575; MUID:93371598; PMID:769834
A;Accession: PN0575

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 19-30 <ICH1>
A;Accession: PN0582
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 35-61 <ICH2>
A;Accession: PN0588
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 62-106 <ICH3>
R;O'Malley, K.L.; Anhalt, M.J.; Martin, B.M.; Kelsoe, J.R.; Winfield, S.L.; Ginnis, E.I.
Biochemistry 26, 291-2914, 1987
A;Title: Isolation and characterization of the human tyrosine hydroxylase gene: identification number: 152296; MUID:88107612; PMID:2892328
A;Accession: I52396
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-61 <OMA>
A;Cross-references: GB:MB18116; NID:9329533; PIDN:AAA77649.1; PID:G1004335
R;Kobayashi, K.; Kaneda, N.; Ichinose, H.; Kishi, F.; Nakazawa, A.; Kurokawa, Y.; Fujita
Nuclic Acids Res. 15, 6733, 1987
A;Title: Isolation of a full-length cDNA clone encoding human tyrosine hydroxylase type
A;Reference number: I38340; MUID:87316931; PMID:2888085
A;Accession: I38340
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-10, 35-528 <KOBA4>
A;Cross-references: EMBL:Y00414; NID:G31726; PIDN:CAA68472.1; PID:G37127
R;Ginnis, E.I.; Rehavi, M.; Martin, B.M.; Waller, M.; O'Malley, K.L.; LaMarca, M.E.; McAll
J. Biol. Chem. 263, 7406-7410, 1988
A;Title: Expression of human tyrosine hydroxylase cDNA in invertebrate cells using a bac
A;Reference number: 155232; MUID:88213428; PMID:2896667
A;Accession: I55282
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-10, 62-64 <GIN1>
A;Cross-references: GB:MB20911; NID:9339636; PIDN:AAA61167.1; PID:G339637
A;Accession: I10056
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-34, 62-64 <GIN2>
A;Cross-references: GB:MB20912; NID:9339642; PIDN:AAA61168.1; PID:G339643
C;Comment: The expression of the four distinct proteins produced by alternate splicing v
C;Genetics:
A;Gene: GDB:TH
A;Cross-references: GDB:119612; OMIM:191290
A;Map position: 11p15.5-11p15.5
A;Introns: 34/3; 61/3; 135/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the 3'-hydroxylation of tyrosine to 3', 4'-dihydroxyphenylalanin
A;Pathway: catecholamine biosynthesis
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: alternative splicing; biotin; catecholamine biosynthesis; iron; metallopro
P1-34_62-528/Product: tyrosine 3-monooxygenase, splice form 4 #status predicted <MAT4>
P1-30_35-528/Product: tyrosine 3-monooxygenase, splice form 3 #status predicted <MAT3>
P1-30_62-528/Product: tyrosine 3-monooxygenase, splice form 2 #status predicted <MAT2>
P1-30_62-528/Product: tyrosine 3-monooxygenase, splice form 1 #status predicted <MAT1>
P8/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predicted
P19/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status pre
P1-183/Binding site: iron (His, His, Glu) #status predicted
P361_366_406/Binding site: iron (His, His, Glu) #status predicted
Query Match 11.6%; Score 220; DB 1; Length 528;
Best Local Similarity 26.7%; Pred. No. 6.2e-10;
Matches 38; Mismatches 104; Indels 36; Gaps 5;
Qy 112 SSREFSLWKS-----VCPRFPLDYLEAFGLSLSDFLDH-----QAVIKPFPELETHF 155
Db 257 AEETATWKEVYTTLKGLYIATHACGEHLIAFAALLERSGYREDNIPQ-EDVSRFLKERTGF 316

Scoring table:	BLOSUM62	Score:	141681	Total number of hits satisfying chosen parameters:	141681	Description
Searched:	141681 seqs, 52070155 residues	Minimum DB seq length:	0	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
		Maximum DB seq length:	2000000000	Post-processing: Minimum Match 0%		
				Maximum Match 100%		
Database :	SwissProt_42:*	Listing first 45 summaries				
Result No.	Score	Match	Length	DB	ID	
1	1886	99.8	362	1	AAAH_CHLNP	Q9z213 chlamydia p
2	265.5	13.6	289	1	PH4H_VIBCH	Q9kb88 vibrio choi
3	235.5	12.5	262	1	PH4H_PSEAB	P4334 pseudomonas
4	231.1	12.2	445	1	TH1_CHICK	P7000 gallus galli
5	230.5	12.2	444	1	TPH1_HUMAN	P1752 homo sapien
6	229.5	12.1	491	1	TY3H_PHASP	P11982 phasianidae
7	227.5	12.0	444	1	TPH1_DAT	P02810 rattus norvegicus
8	226.5	12.0	447	1	TPH1_RABIT	P17532 mus musculus
9	225.5	11.9	444	1	TY3H_ANGAN	P17390 oryctolagrus
10	225.5	11.9	488	1	TY3H_MOUSE	O42091 anguilla anguilla
11	223.5	11.9	498	1	TY3H_MOUSE	P24529 mus musculus
12	223.5	11.8	481	1	TPH2_XENLA	Q92142 xenopus laevis
13	222.3	11.8	498	1	TY3H_RAT	P04177 rattus norvegicus
14	221.5	11.7	490	1	TY3H_BOVIN	P17899 bos taurinus
15	221.1	11.7	275	1	PH4H_RHILLO	Q98722 rhizobium 1
16	220.0	11.6	528	1	TY3H_HUMAN	P07101 homo sapiens
17	219.0	11.6	579	1	TY3H_DROME	P18459 drosophila melanogaster
18	216.5	11.5	465	1	TY3H_SCHEMA	O17446 schistosoma
19	216.5	11.5	490	1	TPH2_HUMAN	Q8WU9 homo sapiens
20	214.5	11.3	453	1	PH4H_RAT	P04176 rattus norvegicus
21	213.5	11.3	452	1	PH4H_HUMAN	P00139 homo sapiens
22	213.5	11.3	485	1	TPH2_RAT	Q8CQ99 rattus norvegicus
23	212.5	11.2	453	1	PH4H_MOUSE	P16331 mus musculus
24	205.5	10.9	488	1	TPH2_MOUSE	Q8CQ92 mus musculus
25	202.0	10.6	313	1	PH4H_RALSO	Q8XJ39 ralstonia eutropha
26	195.0	10.3	297	1	PH4H_CHRVO	P30367 chromobacter violaceus
27	194.0	10.3	452	1	PH4H_DROME	P17276 drosophila melanogaster
28	189.5	10.0	294	1	PH4H_CRAUCHR	Q9afrv7 caenorhabditis elegans
29	178.5	9.4	524	1	TY3H_CAEHEL	P90386 caenorhabditis elegans
30	175.5	9.3	457	1	PH4H_CAEHEL	P90255 caenorhabditis elegans
31	106.5	5.6	506	1	MATK_ARALI	Q9gj63 arabis alpina
32	106.5	5.6	1501	1	NINC_DROME	P10576 drosophila melanogaster
33	106.5	5.6	504	1	MATK_CARAN	Q9gt55 cardamine a

ALIGNMENTS						
RESULT 1						
ID	AAAHH_CHLNP	STANDARD;	PRT;	362	AA.	
AC	Q9Z6L5;					
DT	28-FEB-2003	(Rel. 41, Created)				
DT	28-FEB-2003	(Rel. 41, Last sequence update)				
DT	10-OCT-2003	(Rel. 42, Last annotation update)				
DE	Probable aromatic amino acid hydroxylase (EC 1.14.16.-).					
GN	CPN1046 OR CP0006 OR CPB1046 OR CPB1086.					
OS	Chlamydia pneumoniae (Chlamydophila pneumoniae).					
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.					
OX	NCBI_TaxID:83558;					
RN	[1] - TaxID:83558;					
RP	SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.					
RX	STRAIN=CWL029;					
RA	Medline=93206606; PubMed=10192388;					
RA	Kalmann S., Mitchell W., Marat J., Pan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";					
RA	RNU. Genet. 21:385-389(1999).					
[12]						
RN	SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.					
RX	Medline=20150255; PubMed=10684935;					
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickley E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J.J., Khoruri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";					
RT	"Comparison of whole genome sequences of Chlamydia pneumoniae and CWL029 from USA."					
RL	Nucleic Acids Res. 28:1397-1406(2000).					
[13]						
RN	SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.					
RX	Medline=20150349; PubMed=10871362;					
RA	Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";					
RA	RT "Comparison of whole genome sequences of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";					
RA	RT Submitted (MAY-2002) to the ENBL/GenBank/DDBe databases.					
CC	-1- COFACTOR: Binds 1 ferrous ion (By similarity).					
CC	-1- SIMILARITY: Belongs to the biotin-dependent aromatic amino acid hydroxylase family.					
[14]						
RN	SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.					
RC	Gang M.M., Schlueter A., Muhldorffer I., Bansch K.W., Schaefer K.P., Schneider S., Pohl T., Essig A., Marre R., Melchers K.; "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";					
RA	RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";					
RA	RT Submitted (MAY-2002) to the ENBL/GenBank/DDBe databases.					
CC	-1- COFACTOR: Binds 1 ferrous ion (By similarity).					
CC	-1- SIMILARITY: Belongs to the biotin-dependent aromatic amino acid hydroxylase family.					
[15]						
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CG MEDLINE=20406833; PubMed=10952301;
 CC Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L.,
 CC Haff D.H.; Hickey E.K.; Peterson J.D.; Umamaham L.A.,
 CC Gill S.R.; Nelson K.E.; Read T.D.; Tettelin H.; Richardson D.,
 CC Ermalava M.D.; Vamathevan J.; Bass S.; Qin H.; Dragoi I.,
 CC McDonald L.; Utterback T.; Fleischmann R.D.; Nierman W.C.,
 CC Salzberg S.L.; Smith H.O.; Colwell R.R.; Mekalanos J.J.; Venter J.C.,
 CC Fraser C.M.,
 EMBL "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 PIR: C86621; C86621.
 DR Nature 406:477-483 (2000).
 DR RL
 DR PIR: E72002; E72002.
 DR TIGR: CP0806.
 DR InterPro IPR001273; Aaa_hydroxylase.
 DR PRIMTS; PR00372; FYWHDYRDXASE.
 DR PRINTS; PR002559; Aaa_hydroxylase; 1.
 DR PRODom; PS00367; BIOPTERIN_HDROXYK_1.
 DR Oxidoreductase; Monooxygenase; Iron_Complete proteome.
 DR IRON (POTENTIAL).
 FT METAL 200 IRON (POTENTIAL).
 FT METAL 205 IRON (POTENTIAL).
 FT CONFLICT 131 E -> D (IN REF 4).
 SQ SEQUENCE 362 AA; 42513 MW; 01B8BB4FEB593B CRC64;
 Query Match 99.8%; Score 1886; DB 1; Length 362;
 Best Local Similarity 99.7%; Pred. No. 2..3e-140;
 Matches 361; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHYCERTIDPKTKLKAIRKLSLDFQNSQSLQRAYSTPSYRJILQKENKEQALA 60
 Db 1 MYCERILDPKYLKAKLIRKLSLDFQNSQSLQRAYSTPSYRJILQKENKEQALA 60
 Qy 61 RHKCISLEFFKQNLFVHLISLKNQREGCSIDMAVYSTPFVNRLWYRLLSSRLWS 120
 Db 61 RHKCISLEFFKQNLFVHLISLKNQREGCSIDMAVYSTPFVNRLWYRLLSSRLWS 120
 Qy 61 YCPRFEDYLEAFLGLSDPLDHOAVIKKFELTFSYPSVGFAVHQYISLQLDRYFP 180
 Db 121 YCPRFEDYLEAFLGLSDPLDHOAVIKKFELTFSYPSVGFAVHQYISLQLDRYFP 180
 Qy 181 ASYMPYLDKDNESLTPLDHLIGHVPMILHHSSEFFINGLRLEFKVILKQALPSKKQ 240
 Db 181 ASYVRTLDDNFSLTTPDILHDLIGHVPMILHHSSEFFINGLRLEFKVILKQALPSKKQ 240
 Qy 241 RIQIQLQNLIAIVRCFWPTVESSLIEENGRKAYGAVLISSQELGAFTNVRVPLE 300
 Db 241 RIQIQLQNLIAIVRCFWPTVESSLIEENGRKAYGAVLISSQELGAFTNVRVPLE 300
 Qy 301 DQIIRLPNTSTPQTBLTSLRHFDELTSKLEWMDQGLLESIPLYNQEKYLSSFEVL 360
 Db 301 DQIIRLPNTSTPQTBLTSLRHFDELTSKLEWMDQGLLESIPLYNQEKYLSSFEVL 360
 Qy 361 CQ 362
 Db 361 CQ 362

RESULT 2
 PH4H_VIBCH STANDARD; PRT; 289 AA.
 ID PH4H_VIBCH
 AC Q9KUB8;
 DT 28-Feb-2003 (Rel. 41, Created)
 DT 28-Feb-2003 (Rel. 41, Last sequence update)
 DT 10-Oct-2003 (Rel. 42, Last annotation update)
 DE Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
 monooxygenase).
 GN PHA OR VCA0828.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 STRAIN=El Tor N16961 / Serotype O1;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC

RX RX
 RA RA
 RA Hedson R.J.; Haft D.H.; Hickey E.K.; Peterson J.D.; Umamaham L.A.,
 RA Gill S.R.; Nelson K.E.; Read T.D.; Tettelin H.; Richardson D.,
 RA Ermalava M.D.; Vamathevan J.; Bass S.; Qin H.; Dragoi I.,
 RA McDonald L.; Utterback T.; Fleischmann R.D.; Nierman W.C.,
 RA Salzberg S.L.; Smith H.O.; Colwell R.R.; Mekalanos J.J.; Venter J.C.,
 RA Fraser C.M.,
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483 (2000).
 DR
 CC !- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
 CC L-Lysroline + 4-alpha-hydroxytetrahydrobiopterin.
 CC |- COFACTOR: Binds 1 ferrous ion (By similarity).
 CC |- PATHWAY: Catabolism of Phenylalanine; first (rate-limiting) step.
 CC |- SIMILARITY: Belongs to the biotin-dependent aromatic amino acid
 CC hydroxylase family.
 CC
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 EMBL; AE004410; AAFF96726.1; -
 DR PIR; D82413; D82413.
 DR HSSP; P04177; ITOH.
 DR TIGR; VCA0828.
 DR InterPro; IPR001273; Aaa_hydroxylase.
 DR Pfan; PR00351; biotin; Phenylalanine.
 DR PRNTS; PR00372; FYWHDYRDXASE.
 DR Problem; PD00559; Aaa_hydroxylase; 1.
 DR TIGRFAMS; TIGR01267; Phe4hydro mono; 1.
 DR PROSITE; PS00367; BIOPERTIN_HYDROXYL_1.
 DR KW Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron; Complete proteome.
 KW Complete proteome.
 FT METAL 144 IRON (POTENTIAL).
 FT METAL 149 IRON (POTENTIAL).
 SEQENCE 289 AA; 33445 MW; 2D68B1C6B31D51 CRC64;
 Qy Query Match 13.6%; Score 256.5; DB 1; Length 289;
 Qy Best Local Similarity 25.6%; Pred. No. 5.4e-13;
 Matches 65; Conservative 56; Mismatches 108; Indels 25; Gaps 6;
 Qy 106 LWYRLLSSRFSLNKSYCBPFEDYLEAFLGLLESIPLYNQEKYLSSFEVL 164
 Db 49 VWHHEIITRQEYVKTTRACQAYLGLNNLNLPDTRLPLPEINVRQETGWQVEPVALI 108
 Qy 165 APHQYLSLQDRYPIASVMTLQDKDNESLTPLDHLIGHVPMILHHSSEFFINGLR 224
 Db 109 SFDRFFALLADKKEPPVATLRRREEFDYIQLQEPDFFHBYVGHCAMLTPDFAFTHYVQQL 168
 Qy 225 FTKYIEKVQALPSKQRQIOTLQNLIAIVRCFWPTVESSLIEENGRKAYGAVLISSFEVL 284
 Db 169 GAKATPKERSY-----LARLTFETVFGLVQEGQKTYGGGLSSPGE 212
 Qy 285 LGHAFTDNV-RVPLPLEDQDQIIRLPNTSTPQTBLTSLRHFDELTSKLEWMDQGLLESIPLYNQEKYLSSFEVL 338
 Db 213 TLYABESTI-PKRBPDPIMQVLRPYR1DQMIPYVVLQDLSQYQQLORDNAUWQAMQ 272
 Qy 339 QGLIESIPILYNEQK 352
 Db 273 DGLLP--PLFQPKE 284
 RESULT 3
 PH4H_PSEAE STANDARD;
 ID PH4H_PSEAE
 AC P4334;
 DT 01-Nov-1995 (Rel. 32, Created)

Db	174	WGTVEREILNKLYPTAACR--EYLNKLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR	230	Query Match Score 229.5; DB 1; Length 491;
Qy	159	PVGFUVAHQYLSSLQDRAFTPLASVMTIDKDNFESTLTPDLIHDLLGHVPLHPSSEFF	218	Best Local Similarity 29.1%; Pred. No. 1.4e-10; Matches 66; Conservative 34; Mismatches 100; Indels 27; Gaps 4;
Db	231	PVAGYLSPRDFESGLAFTVPHCTQYTHSSDPEYTPEPDTCHELLGVPLIAEPAOFIS	290	Qy 107 WYRLSSRFSLNKSYCPRFELDYLEAFGILSDFLDH-----QAIKFFLETHFSYY 158 Db 226 WKEVTSLKSLYPHTACK---EYLFANLLEKCGYNENNIPOLEEVSRFLKERTGFLR 282
Qy	219	INNGRLFLVIEKVQALPSKKKQIQTLOSSNLIAIVRCENFTVEGLIENHGRKAYGAVL	278	Qy 159 PVSGRAVAPHOYLSSLQDRAFTPLASVMTIDKDNFESTLTPDLIHDLLGHVPLHPSSEFF 218 Db 283 PVRGLISARDPLASIAFRQCTQYIHRASSPSPHSPPDCHELLGVPMADKTPAFAFS 342
Db	291	QEIG----LASIGSEEAVQKAT-----CYFPTYEGFLCKQDGOLRVEGAGL	334	Qy 219 INMGRBLFTVKVIEKQVQLPSKKQIQTQSNLIAIVRCENFTVEGLIENHGRKAYGAVL 278 Db 343 QDIG----LASIGTDEIEKIAL-----WFTVFGLCHQNGIVKAYGAGL 386
<hr/>				
RESULT 6				
TYH_PHASP		STANDARD	PRT	491 AA.
AC	P11962;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DE	Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).			
GN	[1]			
SEQUENCE FROM N.A.				
RP	SEQUENCE ADRENAL gland;			
RX	TISSUE=Adrenal gland; MEDLINE=88089390; PubMed=2447231;			
RA	Fauquet M., Grima B., Lamouroux A., Mallet J.; Cloning of quail tyrosine hydroxylase; amino acid homology with other hydroxylases discloses functional domains.";			
RT	RT			
RT	J. Neurochem. 50:142-148 (1988).			
RN	[1]			
CC	-1- FUNCIONES: Plays an important role in the physiology of adrenergic neurones.			
CC	-1- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.			
CC	-1- COFACTOR: Ferrous ion.			
CC	-1- ENZYME REGULATION: Phosphorylation leads to an increase in the catalytic activity.			
CC	-1- PATHWAY: Catecholamine biosynthesis; first step.			
CC	-1- SIMILARITY: Belongs to the bipterin-dependent aromatic amino acid hydroxylase family.			
CC	-----			
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CC	-----			
DR	EMBL: M24778; AAA4914.1; -.			
DR	PIR: A28522; A2852.			
DR	HSSP: P04177; 1TOH.			
DR	InterPro: IPR001273; Aaa_hydroxylase.			
DR	InterPro: IPR005962; Tyr_3-monox.			
DR	PFam: PF00351; bioperin_H.			
PRINTS:	PR00372; FWHYDPLXASE.			
DR	ProDom: PD002559; Aaa_hydroxylase; 1.			
DR	TIGRFams: TIGR01269; Ty_3-monoox; 1.			
DR	PROSITE: PS00367; BIOPTEN HYDROXYL.			
DR	Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron; Neurotransmitter biosynthesis; Phosphorylation (BY PHOSPHORYLATION).			
KW	KW			
KW	Neurotransmitter biosynthesis; Phosphorylation (BY PHOSPHORYLATION).			
PT	MOD RES 40	40		
PT	DOMAIN 51	55		
PT	METAL 324	324		
PT	METAL 329	329		
PT	METAL 369	369		
SQ	*SEQUENCE 491 AA; 56066 MW; AFB363220F700A0 CRC64;			

CG M28000; AAA42262; 1; -.
DR EMBL; X53501; CRA3759; 1; -.
DR PIR; JI0034; WIRTW.
DR HSSP; P04177; ITOH.
DR IPR001273; Aaa_hydroxylase.
DR InterPro; IPR002912; ACT.
DR InterPro; IPR005963; Tyr_5_monoxx.
DR Pfam; PF001642; ACT; 1.
DR Pfam; PF00051; biotin_H; 1.
DR PRINTS; PRO0372; FYWHDYKXASE.
DR PRODOM; PDO002559; Aaa_hydroxylase; 1.
DR TIGRFAMS; TIGR01270; Trp_5_monoxx; 1.
DR TIGRFAMS; TIGR01271; BIOPTERIN_HYDROXYL.
DR Oxidoreductase; Monoxygenase; Serotonin biosynthesis; Iron; KW
KW Phosphorylation. PHOSPHORYLATION (BY PKA) (POTENTIAL).
DR Phosphorylation.
DR MOD_RES 58 58 IRON (BY SIMILARITY).
DR METAL 272 272 IRON (BY SIMILARITY).
DR METAL 277 277 IRON (BY SIMILARITY).
DR METAL 317 317 IRON (BY SIMILARITY).
SQ SEQUENCE 444 AA; C3CF54572/CC825 CRC64;
Query Match. Score 12.0%; Best Local Similarity 27.4%; Pred. No. 1.7e-10; Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps 4;
Qy 107 WYRLSSRSFLWKSYCPRFELDYEARGLSIDFLDH----QAVIKFFPELETHFSYY 158
Db 174 WGTFIREFLNKLYTHACR--EYLRLNPLSLRYCGREDNYQLEDVSNFKERTFESIR 230
Qy 159 PVSGFVAPHOYLISLQDRYFPIASVMRTLDKDNFSLTPDLDLHIGHPMLHPSSEFP 218
Db 231 PVAGYLSPPDFLSCLAFLPFRHCTQVYHS SDDPLYTPDPDTCHLLGHVPLAEPSPQAQS 290
Qy 219 INMGRLFVTKVQALPSKQPIOTLQNSNLAVRCFWFTVSGLLENHGRKAYGAVL 278
Db 291 QEIG-----LASLGSAEETVQKLAT-----CYFFTVEGLCKQDGQLRVFGAGL 334
Qy 279 ISSPQELGHAFIDNVRVILEPDLQDIIIRLFNTSTPQETLFSIRHDELVE 328
Db 335 LSSTSELRAHLSGHAKVKFDPRVACKQECLITSFQDVYFVSESFEDAKE 384
RESULT 8
TPH1_MOUSE STANDARD; PRT; 447 AA.
ID TPH1_MOUSE ID_TPH1_RABBIT STANDARD; PRT; 444 AA.
AC P17322; Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophan 5-hydroxylase 1 (EC 1.14.16.4) (Tryptophan 5-monooxygenase 1).
GN TPH1 OR TPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurogathi; Murinae; Mus.
NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RN MEDLINE=90243261; PubMed=2110547;
RN Stoll J., Kozak C.A., Goldman D.; "Characterization and chromosomal mapping of a cDNA encoding tryptophan hydroxylase from a mouse mastocytoma cell line.";
RN Genomics 7:88-96(1990)
RN CATALYTIC ACTIVITY: L-tryptophan + tetrahydrobiopterin + O(2) = 5-hydroxy-L-tryptophan + 4-alpha-hydroxytetrahydrobiopterin.
RN COFACTOR: Ferrous ion.
RN PATHWAY: Serotonin biosynthesis; first step.
RN PATHWAY: Melatonin biosynthesis; first step.
RN SUBUNIT: Multimer of identical subunits.
RN SIMILARITY: Belongs to the bipterin-dependent aromatic amino acid hydroxylases.;"
CC SEQUENCE FROM N.A.

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CC EMBL; J04758; AAA63401; 1; -.
DR PIR; A34582; A34582.
DR HSSP; P04177; ITOH.
DR MGDB; MGT; 9B196; Tph1.
DR InterPro; IPR001273; ACT.
DR InterPro; IPR002912; ACT.
DR InterPro; IPR005963; Tyr_5_monoxx.
DR InterPro; IPR005963; Tyr_5_monoxx.
DR Pfam; PP01812; ACT; 1.
DR Pfam; PF00351; biotin_H; 1.
DR PRINTS; PRO0372; FYWHDYKXASE.
DR PRODOM; PDO00559; Aaa_hydroxylase; 1.
DR TIGRFAMS; TIGR01270; Trp_5_monoxx; 1.
DR PROSITE; PS00367; BIOPTERIN_HYDROXYL.
DR PROSITE; PS00367; BIOPTERIN_HYDROXYL.
DR Cricetomys oryzivorus; Monooxygenase; Serotonin biosynthesis; Iron; KW
KW Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron; KW
KW Phosphorylation.
DR Phosphorylation.
DR MOD_RES 61 61 IRON (BY SIMILARITY).
DR METAL 275 275 IRON (BY SIMILARITY).
DR METAL 280 280 IRON (BY SIMILARITY).
DR METAL 320 320 IRON (BY SIMILARITY).
DR SEQUENCE 447 AA; 51343 MW; 16C839F22A13BBCA CRC64;
Query Match. Score 226.5; DB 1; Length 447;
Best Local Similarity 27.4%; Pred. No. 2.1e-10; Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps 4;
Qy 107 WYRLSSRSFLWKSYCPRFELDYEARGLSIDFLDH----QAVIKFFPELETHFSYY 158
Db 177 WGTFIREFLNKLYTHACR--EYLRLNPLSKYCGYREDNIPQLEDVNFLLKERTGFSIR 233
Qy 159 PVSGFVAPHOYLISLQDRYFPIASVMRTLDKDNFSLTPDLDLHIGHPMLHPSSEFP 218
Db 234 PVAGYLSPPDFLSCLAFLPFRHCTQVYHS SDDPLYTPDPDTCHLLGHVPLAEPSPQAQS 293
Qy 219 INMGRLFVTKVQALPSKQPIOTLQNSNLAVRCFWFTVSGLLENHGRKAYGAVL 278
Db 294 QEIG-----LASLGSAEETVQKLAT-----CYFFTVEGLCKQDGQLRVFGAGL 334
Db 295 ISSPQELGHAFIDNVRVILEPDLQDIIIRLFNTSTPQETLFSIRHDELVE 328
Db 338 LSSISLKLHSLGHAKVKFDPKIAKQECLITSFQDVYFVSESFEDAKE 387
RESULT 9
TPH1_RABBIT STANDARD; PRT; 444 AA.
ID TPH1_RABBIT ID_TPH1_RABBIT STANDARD; PRT; 444 AA.
AC P17290; Q9523; Rel. 15, Created)
DT 01-APR-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophan 5-hydroxylase 1 (EC 1.14.16.4) (Tryptophan 5-monooxygenase 1).
GN TPH1 OR TPH.
OS Oryctolagus cuniculus (Rabbit).
OC Bukaoyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
OC NCBITaxon=9986;
RN [1] SEQUENCE FROM N.A.
RN MEDLINE=8728963; PubMed=3475690;
RN Grenett H.E., Ledley F.D., Reed L.L., Woo S.L.C.; RT "Full-length cDNA for rabbit tryptophan hydroxylase: functional domains and evolution of aromatic amino acid hydroxylases.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5530-5534 (1987).
RN [2] SEQUENCE FROM N.A.

Page 7

Dr 383 LLSSYGEVLVHSLSDEPERREFDPEAAAEPYQDQNYQSYYFVSESFTDAE 433

RESULT 11

TY3H_MOUSE STANDARD; PRT; 498 AA.

ID AC P24529; (Rel. 21; Created)

DT 01-MAR-1992 (Rel. 21; Last sequence update)

DT 01-MAR-1992 (Rel. 21; Last annotation update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DB GN TH.

OS Mus musculus (Mouse); Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

OX NCBI_TAXID=10090;

[1]

RN SEQUENCE FROM N.A.; PubMed=1674869;

RX MEDLINE=91248263;

RA Ichikawa S., Sasaoka T., Nagatsu T.; Primary structure of mouse tyrosine hydroxylase deduced from its cDNA. " Biochem. Biophys. Res. Commun. 176:1610-1616(1991).

RN [2]

RP SEQUENCE OF 1-30 FROM N.A.

RC STRAIN=BALB/C,

RA Morgan W.W.; Bermudez J.; Sharp Z.D.; Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

CC -I- FUNCTION: Plays an important role in the physiology of neurons.

CC -I- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropyridine + H₂O.

CC -I- COFACTOR: Ferrous ion.

CC -I- PATHWAY: Phosphorylation leads to an increase in the catalytic activity.

CC -I- PATHWAY: Catecholamine biosynthesis; first step.

CC -I- SIMILARITY: Belongs to the bioperin-dependent aromatic amino acid hydroxylase family.

CC -----

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CC -----

DR ENMB; M6200; AAA4043; -.

DR ENMB; X53503; CAA37580; -.

DR PIR; JNC68; JNO068.

DR HSSP; P04177; 1TOH.

DR MGD; MG3:98735; Th.

DR GO; GO:0006885; P-dopamine biosynthesis from tyrosine; IDA.

DR GO; GO:0007507; P:heart development; IMP.

DR GO; GO:0008016; P:regulation of heart rate; IMP.

DR InterPro; IPR001273; Aaa hydroxylase.

DR InterPro; IPR05921; Tyr₃-monox.

DR Pfam; PF00351; bipterin_H_1.

DR PRINTS; PR00172; FYWHDYKXLE.

DR TIGRFAMS; TIGR01269; Tyr₃-monoox; 1.

DR PROSITE; PS00367; BIOPTERIN HYDROXYL.

KW Catecholamine biosynthesis; Oxidoreductase; Monoxygenase; Iron; Neurotransmitter; Phosphorylation.

FT MOD_RES 19 19

FT MOD_RES 31 31

FT MOD_RES 40 40

FT DOMAIN 51 59

FT METAL 331 331

FT METAL 336 336

FT METAL 376 376

SQ SEQUENCE 498 AA; 555992 MW; 62790179664; F6DC6 CRC64;

Query Match 11.9%; Score 225.5; DB 1; Length 498;

Best Local Similarity 27.5%; Pred No. 2.8e-10; Mismatches 101; Indels 31; Gaps 5;

Matches 66; Conservative 42; Mi matches 101; Indels 31; Gaps 5;

QY 107 WYRLSSRFSLWSYCYCPRFELDYLAEGFLSDFLDH-----QAVIKPFELTHEFSYY 158

Db 233 WKEVYATLKGLYATHACR--EHLEAQQLERYCGYREDSTIPQLEDVSHFLKERTGQLR 289

QY 159 PYSGFVAPHOYLSSLQQRYFPTASVNTLKDNTSUTPDJLTHLGHPPLHPPFSEFF 218

Db 290 PVALGLSARDFLASLARVFQOTQYTRASSPMHSBPDCHELLGHVPMADRIFQAQS 349

QY 219 INMGRILFTKVIEKVQALPSKKORIQTQNSNLIAIVRCFWETVESSLIEHENGRKAYGAVL 278

Db 350 QDIG-----LASTGASDEBIEKLST-----VYWFWVEFGLKONGELRAYAGGL 393

QY 279 ISSPQEGLGHAFIDNVRLVPLIEDQIQLPNTSTQETLTSIRHF---DELVELTSKLE 334

Db 394 LSSYGEPLLHSLSSEPEYTRAFFDPTAVQVYQDQTVQPVYFSESFSDAKLNRNTASRIQ 453

RESULT 12

TPH_XENIA STANDARD; PRT; 481 AA.

ID TPH_XENIA O92142; (Rel. 36; Created)

AC DT 15-JUL-1998 (Rel. 36; Last sequence update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DE TRYPTOPHAN 5-hydroxylase (EC 1.14.16.4) (TRYPTOPHAN 5-monoxygenase).

GN TPH.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Bercachia; Anura; Meobatrachia; Pipidae; Xenopodinae; Xenopus.

OC NCBI_TAXID=3355;

RN [1] --

RP SEQUENCE FROM N.A.

RC TISSUE=retina;

RX MEDLINE=94266419; PubMed=81189245;

RA Green C.B.; Besnard J.C.;

RT "Tryptophan hydroxylase expression is regulated by a circadian clock in Xenopus laevis retina." J. Neurochem. 62:2420-2428(1994).

RL J. Neurochem.

CC -I- CATALYTIC ACTIVITY: L-tryptophan + tetrahydrobiopterin + O(2) = 5-hydroxy-L-tryptophan + 4-alpha-hydroxytetrahydrobiopterin.

CC -I- COFACTOR: Ferrous ion.

CC -I- PATHWAY: Serotonin biosynthesis; first step.

CC -I- SUBUNIT: Multimer of identical subunits (By similarity).

CC -I- SIMILARITY: Belongs to the bioperin-dependent aromatic amino acid hydroxylase family.

CC -----

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CC -----

CC DR PIR; 151567; 151567.

CC DR HSSP; P04177; 1TOH.

CC DR InterPro; IPR01273; Aaa_Hydroxylase.

CC DR InterPro; IPR012912; ACT.

CC DR InterPro; IPR005983; Tyr_5_monoX.

CC DR Pfam; PF01842; ACT; 1.

CC DR Pfam; PF00351; bipterin_H_1.

CC DR PRINTS; PR00372; FYWHDYKXLE.

CC DR PRODOM; PD02559; Aaa_hydroxylase; 1.

CC DR TIGRFAMS; TIGR01270; Tyr₃-monoox; 1.

CC DR PROSITE; PS00367; BIOPTERIN HYDROXYL.

CC DR DR PIR; 1515679; AAA1306; 1; -.

CC DR DR HSSP; P04177; 1TOH.

CC DR DR InterPro; IPR01273; Aaa_Hydroxylase.

CC DR DR InterPro; IPR012912; ACT.

CC DR DR InterPro; IPR005983; Tyr_5_monoX.

CC DR DR Pfam; PF01842; ACT; 1.

CC DR DR Pfam; PF00351; bipterin_H_1.

CC DR DR PRINTS; PR00372; FYWHDYKXLE.

CC DR DR PRODOM; PD02559; Aaa_hydroxylase; 1.

CC DR DR TIGRFAMS; TIGR01270; Tyr₃-monoox; 1.

CC DR DR PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

Oxidoreductase; Monoxygenase; Serotonin biosynthesis; Iron.
 METAL 309 IRON (BY SIMILARITY).
 PT 314 IRON (BY SIMILARITY).
 METAL 354 IRON (BY SIMILARITY).
 FT SEQUENCE 481 AA; 55406 MW; 6852C33EFF8DEBA0 CRC64;
 CC -|- FUNCTION: Plays an important role in the physiology of adrenergic
 neurons.
 CC -|- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-
 dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
 CC -|- COFACTOR: Ferrous ion.
 CC -|- ENZYME REGULATION: Phosphorylation leads to an increase in the
 catalytic activity.
 CC -|- PATHWAY: Catecholamine biosynthesis; first step.
 CC -|- SUBPATHWAY: Homotetramer.
 CC -|- SIMILARITY: Belongs to the bipterin-dependent aromatic amino acid
 hydroxylase family.
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 or send an email to license@isb-sib.ch).
 CC ---
 DR EMBL; M10244; AAA42257.1;
 DR EMBL; L22651; AAA42258.1;
 DR PIR; A00510; WHRY.
 DR PDB; 1TCB; 03-JUN-98.
 DR InterPro; IPR01273; Aaa_hydroxylase.
 DR InterPro; IPR01592; FWHYHDXKASE.
 DR PFAM; PF00351; bipterin_H; 1.
 DR PRINTS; PR00372; FWHYHDXKASE.
 DR PRODOM; PD002559; Aaa_hydroxylase; 1.
 DR TIGRFAM; TIGR01369; Tyr_3_monoxx; 1.
 DR PROSITE; PS00367; BIOPTERIN_HYDROXYL_1.
 KW Catecholamine biosynthesis_Oxidoreductase; Monoxygenase; Iron;
 KW Neurotransmitter biosynthesis_Phosphorylation; 3D-structure.
 FT MOD RES 19 19 PHOSPHORYLATION (BY CAMK2).
 FT MOD RES 31 31 PHOSPHORYLATION (BY PKA).
 FT MOD RES 4 40 PHOSPHORYLATION (BY PKA).
 FT DOMAIN 51 59 POLY-ALA.
 FT METAL 331 331 IRON.
 FT METAL 336 336 IRON.
 FT METAL 376 376 IRON.
 FT STRAND 170 170
 FT HELIX 171 176
 FT TURN 190 191
 FT TURN 193 196
 FT HELIX 198 213
 FT TURN 216 217
 FT HELIX 227 247
 FT STRAND 248 248
 FT HELIX 250 262
 FT STRAND 266 266
 FT TURN 267 268
 FT STRAND 269 269
 FT HELIX 273 283
 FT TURN 284 284
 FT STRAND 287 290
 FT HELIX 297 304
 FT TURN 305 307
 FT STRAND 308 311
 FT TURN 318 319
 FT STRAND 321 322
 FT HELIX 329 335
 FT TURN 336 336
 FT HELIX 337 340
 FT TURN 341 341
 FT HELIX 343 356
 FT TURN 357 358
 FT HELIX 361 372
 FT TURN 373 377
 FT STRAND 379 382
 FT TURN 383 384
 FT STRAND 385 388
 FT HELIX 391 394
 CC ---
 RESULT 13
 TY3H RAT ID TY3H RAT STANDARD; PRT; 498 AA.
 AC P04177;
 AC 04 ; Created
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 20-MAR-1987 (Rel. 04, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
 GN TH.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID:10116;
 RN [1] SEQUENCE FROM N.A., MEDLINE=85113247; PubMed=857492;
 RN Grima B., Lamouroux A., Blanot P., Facon Biguet N., Mallet J.;
 RN "Complete coding sequence of rat tyrosine hydroxylase mRNA.",
 RN Proc. Natl. Acad. Sci. U.S.A. 82:617-621(1985).
 RN [2] SEQUENCE FROM N.A., MEDLINE=91170235; PubMed=16723315;
 RN Haycock J.W., Haycock D.A.;
 RN "Tyrosine hydroxylase in rat brain dopaminergic nerve terminals.
 RN Multiple-site phosphorylation in vivo and in synaptosomes.",
 RN J. Biol. Chem. 266:5650-5657(1991).
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-498.
 RN MEDLINE=97312896; PubMed=9228951;
 RN Goodwill K.E., Sabatier C., Marks C., Raag R., Fitzpatrick P.F.,
 RN Stevens R.C.;
 RN "Crystal structure of tyrosine hydroxylase at 2.3 A and its
 RN implications for inherited neurodegenerative diseases.",
 RN Nat. Struct. Biol. 4:578-585 (1997).
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 160-498.
 RN MEDLINE=9846038; PubMed=9153429;
 RN Goodwill K.E., Sabatier C., Stevens R.C.;
 RN "Crystal structure of tyrosine hydroxylase with bound cofactor
 RN analogue and iron at 2.3 A resolution: Self-hydroxylation of Phe300
 RN and the pterin-binding site.",
 RN Biochemistry 37:13437-13445 (1998).

QY	282	PAGLISARDFLASLAFRVFOCTQYIRHSSPMSPEFCCHELLGHPMLADRTPAQFS	341
QY	219	INNGRLFTKVIKEVQALPKKORIQTQLQNLATVRCFWFTVSGLINHEGRKAYGAVL	278
QY	342	QDIG-----LASLGUSDEETEKLST-----LWVTFEGLKONGEVKAYGAGL	385
QY	279	ISSQELGHAFIDNVRVLELUDLDIRFNTSTPQEUTFSRHF---DELYELTSKLE	334
QY	386	LSSYGEELLSLSELSEPEIRADPDAAAVQYQDCRYQPVTFVSESFSADKDLRSYASRIL	445
RESULT 15			
PH4H_RHIO		STANDARD;	PRT;
AC	Q9ED72;		275 AA.
DDT	28-FEB-2003	(Rel. 41; Created)	
DT	28-FEB-2003	(Rel. 41; Last sequence update)	
DT	10-OCT-2003	(Rel. 42; Last annotation update)	
DE	Phenylalanine 4-hydroxylase (EC 1.14.16.1) (PAH)	(Phe-4-monoxygenase).	
GN	PAH OR MLR4B1.		
OS	Rhizobium loti (Mesorhizobium loti).		
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.		
OX	NCBI_TaxID=381;		
RN	[1]		
SEQUENCE FROM N.A.			
STRIDE=RPPF303099; MEDLINE=21082830; PubMed=11214968;			
MEDLINE=21082830; PubMed=11214968;			
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa A., Ishikawa C., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shindo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti"; DNA Res. 7:331-338 (2000).			
- - CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) = L-tyrosine + 4 alpha-hydroxytetrahydrobiopterin.			
- - COFACTOR: Binds 1 ferrous ion (By similarity).			
- - PATHWAY: Catabolism of phenylalanine: first (rate-limiting) step.			
- - SIMILARITY: Belongs to the biopterin-dependent aromatic amino acid hydroxylase family.			

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DR	EMBL: AP03005; BAB1399_1;		
DR	InterPro: IPR001273; Aaa hydroxylase.		
DR	Intervo; IPR005960; Phenylal4OHaseM.		
DR	Pfam: PF00351; biopterin_H; 1.		
DR	PRINTS; PR000372; FWHYDRLASE.		
DR	ProDom; PDO5555; Aaa_hydroxylase; 1.		
DR	TIGRFAMS; TIGR01267; Phenylhydrox mono; 1.		
DR	PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.		
DR	Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron; Complete proteome.		
FT	KW	Iron	(POTENTIAL).
FT	METAL	135	135
FT	METAL	140	140
SQ	SEQUENCE	275 AA;	31347 MW; BC29D25534BC215 CRC64;
SQ	Query Match	11.7%	Score 221; DB 1; Length 275;
Matches 65; Conservative 40; Mismatches 109; Indels 36; Gaps 6;	Best Local Similarity 26.0%; Pred. No. 3.1e-10;		
90 CSTDMAYSTPFFENRNLMLSSRFLSIWKSICPR-----FPDYLAFGLLSD 138			
22 CBADFTVAD-----YDSDEFQWRTKLRKLAHHSYLDGVYKLGLDR 73			

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OM protein - protein search, using SW model.

Run on: March 25, 2004, 14:10:43 ; Search time 45 Seconds

2538.169 Million cell updates/sec
(without alignments)

Title: US-09-438-185A-1047
Perfect score: 1889
Sequence: 1 VHYCBTLDPKYKILKALKL.....ESIPLYNQEKKYLSGFELVLCQ 362

Scoring table: BLASTM52
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25+*
1: sp_archaea,*
2: sp_bacteria,*
3: sp_fungi,*
4: sp_human,*
5: sp_invertebrate,*
6: sp_mammal,*
7: sp_mhc:
8: sp_organelle,*
9: sp_phage,*
10: sp_Plant,*
11: sp_F rodent,*
12: sp_virus,*
13: sp_vertebrate,*
14: sp_unclassified,*
15: sp_rvirus,*
16: sp_bacteriopl,*
17: sp_archeap,*

SPTREMBL 25+*

1: 543.5 28.8 277 16 Q822G6
2: 243.5 12.9 471 13 Q8AY71
3: 237.5 12.6 491 13 Q9PU40
4: 231.5 12.3 446 11 Q8K3R1
5: 230.5 12.2 264 16 Q87IN0
6: 229 12.1 271 16 Q8EGD8
7: 228.5 12.1 263 16 Q8DSO
8: 226.5 12.0 262 16 Q88EH3
9: 226 12.0 265 16 Q88SL0
10: 224.5 11.9 497 5 Q863T0
11: 223.5 11.8 584 16 Q81LM9
12: 220.5 11.7 584 16 Q81B84
13: 219.5 11.6 296 16 Q8PQZ5
14: 215.5 11.4 453 16 Q91WV1
15: 214 11.3 296 16 Q8PE27
16: 213.5 11.3 452 4 Q8TEY0

ALIGNMENTS

RESULT 1

ID	Q822G6	PRELIMINARY	PRT;	277 AA.
AC	Q822G6;			
DT	01-JUN-2003 (TREMBL1r1,	24, Created)		
DT	01-JUN-2003 (TREMBL1r1,	24, Last sequence update)		
DT	01-OCT-2003 (TREMBL1r1,	25, Last annotation update)		
DE				
GN				
CCAA0716.				
OS	Chlamydophila caviae			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila			
NCBI TaxID=33557;				
RN	[1]			

SEQUENCE FROM N.A.

RP STRAIN=GPIC;
RC PMID=12682364;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brumham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Fedrova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Besan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bayoil P.M.,
Fraser C.M.;
RA "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiaceae.";
RT Nucleic Acids Res.; 31:213-214(2003).
RT EMBL; AE016936; AAP05458.1; --.
DR EMBL; AE016936; AAP05458.1; --.
DR TIGR; CCA0716; --.
DR GO; GO:0005516; F:iron ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0009072; P:aromatic amino acid family metabolism; IEA.
DR GO; GO:0009072; P:aromatic amino acid family metabolism; IEA.
DR PRINTS; PRO0123; AaaHydroxylase.
DR PRODom; PD002559; Aaa hydroxylase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 277 AA; 32100 MW; OAABEEBA4398BB9 CRC64;
Query Match 28.8%; Score 543.51, DB 16, Length 277;
Best Local Similarity 43.0%; Fred. No. 5.3e-39; Mismatches 95; Indexes 1; Gaps 1;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	Q822G6 chlamydophili					
2	Q8AY71 brachydano					
3	Q9PU40 gallus galli					
4	Q8K3R1 mesocricetus					
5	Q87IN0 vibrio para					
6	Q8EGD8 shewaneilla					
7	Q8DSO vibrio vuln					
8	Q88EH3 pseudomonas					
9	Q88SL0 pseudomonas					
10	Q863T0 schistosoma					
11	Q81LM9 bacillus an					
12	Q81B84 bacillus ce					
13	Q8PQZ5 xanthomonas					
14	Q91WV1 mus musculus					
15	Q8PE27 xanthomonas					
16	Q8TEY0 homo sapien					

Q¹ 96 VVSTPFFNRNLWYRLSSRFLWSKSYCPRFLLDYLBAFGLL-SDFLDHQAVIKFFELETH 154
 Q¹ 5 IATPPSNSENVSGALLNLSRPLWKAVCPQVFFEYLALHIVKGSAIDFDIINNLLSKG 64
 Q¹ 155 FSVYPSGFVAPHQYLSLQLDRYPPASVMTLDKNSFLSTPDLLHDQVPHWLHPSF 214
 DB 65 FTLSPQTQEYLPPHENYLPELSQRERPLATQNAVADDDGFSLFPDLTHDVCHPVWLHPEF 124

Q¹ 215 SEFFINNGRLFTKVEKQVQLPSKSKRQIQTOSNLIAIVCFWFTVESGLIENHEGRKAY 274
 DB 125 MKPFPTGQLEKFAIRAKAEKIPEDOPRILNSNALAISRCFWFTVENGILIEQKRAY 184

Q¹ 275 GAVLISSPQELGHAFIDQVNLVRLPFLDQIIRLPFTNSTPQETLFSTRHFDELVLTSKLE 334
 DB 185 GAIISSSTEQLTYTFANDNFVVSPPKTEHIIQRPCNFNSIQTFFIIRDDELNAISEQME 244

Q¹ 335 WMLDQGLESI 345
 DB 245 QFLNQGQLDFI 255

RESULT 2
 Q8AY71 PRELIMINARY; PRT; 471 AA.
 ID Q8AY71; 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DB TRYptophan hydroxylase D1.
 GN TPBD1.
 Brachydanio rerio (Zebrafish) (Danio rerio).
 Buiaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes;
 Cyprinidae; Danio.
 NCBI_TaxID=7955;

SEQUENCE FROM N.A.
 RA Bellipanni G., Rink E., Balliy-Chif L.;
 RT Cloning of two tryptophan hydroxylase genes expressed in the
 hypothalamic region of the developing zebrafish brain.";
 RL Submitted (SBB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF548556; AAN59951.1;
 GO; GO:0016597; Peptidino acid binding; IEA.
 GO; GO:0004506; Ferron ion binding; IEA.
 DR; GO:0009072; Peptidino acid family metabolism; IEA.
 GO; GO:0008152; Peptidino acid family metabolism; IEA.
 DR; GO:0042427; Peptidino acid biosynthesis; IEA.
 InterPro; IPR001273; Aaa hydroxylase.
 InterPro; IPR002912; ACT.
 InterPro; IPR005963; Tyr 5 Monoox.
 PFam; PF01842; ACT_1.
 PFam; PF00351; biotinin_H_1.
 PRINTS; PR00372; FWHYDXLASE.
 TIGR4M; TIGR01270; TEP5 monoox; 1.
 DR; GO:0042427; Peptidino acid family metabolism; IEA.
 GO; GO:0008152; Peptidino acid family metabolism; IEA.
 DR; GO:0009072; Peptidino acid family metabolism; IEA.
 InterPro; IPR001273; Aaa hydroxylase.

Query Match 12.6%; Score 237.5; DB 13; Length 491;
 Best Local Similarity 29.1%; Pred. No. 3.9e-12; Gaps 4;
 Matches 66; Conservative 36; Mismatches 98; Indels 27; Gaps 4;

Q¹ 107 WYRILSRFSRFLWKSICSPRFELDYLEAFLGGLSDFLDH-----QAVIKFFELTHEFTFSYY 158
 DB 226 WKEVYETLTKLYPTACK--EYLEAFNLLEKEFCYNEENNIPQLEEVSRFLKEBTGFQLR 282

Q¹ 159 PVSGFVAPHQYLSLQLDRYPIASUMRTLDKNSFLSTPDLLHDQVPHWLHPSFSEFF 218
 DR 283 PVAGLISARDFLASLAFRVQCTOYRHASSPMHSPEPDQCEHLGHVPMNLADKTEAQFS 342

DB 219 INMGRRLFTKVBERVQALPSKKQRIQTLQSNLIAIVCPNFTVESCLIENHEGRKAYGAVL 278
 DR 343 QDIG-----LASLGTDTDEEKLATL-----YAPTFVFLCRONGIVEBYGAGL 386

Q¹ 117 LWKSICSPRFELDYLEAFLGGLSDFLDH-----QAVIKFFELTHEFTFSYYGVFAHQ 168
 Best Local Similarity 30.9%; Pred. No. 1.1e-12;
 Matches 67; Conservative 37; Mismatches 86; Indels 27; Gaps 4;

DB 223 LYPSHACR--EYLNQNLPLIHKCDSREDNIPOLEDVSFLKERTGFTRVAGYLSR 279
 Q¹ 279 ISSPQELGHAFIDNYVRLPFLDQIIRLPNTSTPQETLFSIRHDFE 325

DB 387 LSYYGELHSLSDPEPVRDFDPDAAAVQYDQNYQPYFVSESSD 433

RESULT 3
 Q9PP40 PRELIMINARY; PRT; 491 AA.
 ID Q9PP40;
 AC Q9PP40_0;
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DB Tyrosine hydroxylase.
 Galus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gallus.
 NCBI_TaxID=9031;

OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ernsberger U.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9606163; PubMed=7577670;
 RA Ernsberger U., Patzke H., Tissies-Seta J.P., Reh T., Goridis C.,
 Rohrer H.;
 RT "The expression of tyrosine hydroxylase and the transcription factors
 c-Phox-2 and Cash-1: evidence for distinct inductive steps in the
 differentiation of chick sympathetic precursor cells.";
 RT Mech Dev. 52:125-136(1995).
 PL EMBL; AJ751387; CAB62388.1. -.
 DR PIR; S40369; S40309.
 DR HSSP; P04177; 1TOH.
 DR GO; GO:0005506; Ferron ion binding; IEA.
 DR GO; GO:0004511; Ferron ion 3-monooxygenase activity; IEA.
 DR GO; GO:0009072; Peptidino amino acid family metabolism; IEA.
 DR GO; GO:00042423; Peptidocholanine biosynthesis; IEA.
 DR InterPro; IPR001273; Tyr_3-hydroxylase.
 DR InterPro; IPR005962; Tyr_3-monoox.
 DR Pfam; PF00351; biotinin_H_1.
 DR PRINTS; PR00372; FWHYDXLASE.
 DR Product; PR002539; Aaa hydroxylase.
 DR TIGR4M; TIGR01269; Tyr_3-monoox.
 DR PROSITE; PS00367; BIOPTERIN_H_1.
 SQ SEQUENCE 491 AA; 53917 MW; 6322F258E746930 CRC64;

Query Match 12.6%; Score 237.5; DB 13; Length 491;
 Best Local Similarity 29.1%; Pred. No. 3.9e-12; Gaps 4;

Matches 66; Conservative 36; Mismatches 98; Indels 27; Gaps 4;

Q¹ 107 WYRILSRFSRFLWKSICSPRFELDYLEAFLGGLSDFLDH-----QAVIKFFELTHEFTFSYY 158
 DB 226 WKEVYETLTKLYPTACK--EYLEAFNLLEKEFCYNEENNIPQLEEVSRFLKEBTGFQLR 282

Q¹ 159 PVSGFVAPHQYLSLQLDRYPIASUMRTLDKNSFLSTPDLLHDQVPHWLHPSFSEFF 218
 DR 283 PVAGLISARDFLASLAFRVQCTOYRHASSPMHSPEPDQCEHLGHVPMNLADKTEAQFS 342

DB 219 INMGRRLFTKVBERVQALPSKKQRIQTLQSNLIAIVCPNFTVESCLIENHEGRKAYGAVL 278
 DR 343 QDIG-----LASLGTDTDEEKLATL-----YAPTFVFLCRONGIVEBYGAGL 386

Q¹ 117 LWKSICSPRFELDYLEAFLGGLSDFLDH-----QAVIKFFELTHEFTFSYYGVFAHQ 168
 Best Local Similarity 30.9%; Pred. No. 1.1e-12;
 Matches 67; Conservative 37; Mismatches 86; Indels 27; Gaps 4;

DB 223 LYPSHACR--EYLNQNLPLIHKCDSREDNIPOLEDVSFLKERTGFTRVAGYLSR 279
 Q¹ 279 ISSPQELGHAFIDNYVRLPFLDQIIRLPNTSTPQETLFSIRHDFE 325

DB 387 LSYYGELHSLSDPEPVRDFDPDAAAVQYDQNYQPYFVSESSD 433

RESULT 4
 Q8K3R1

DB 229 IERQALPSKHKRQIQTQNSNLIAIVCFWFTVESGLIENHEGRKAYGAVLSSQELGHA 288

Q¹

QBK3R1	PRELIMINARY;	PRT;	446 AA.
AC			
QBK3R1; DT	(TREMBrel. 22, Created)		
01-OCT-2002	(TREMBrel. 22, Last sequence update)		
DT	(TREMBrel. 25, Last annotation update)		
01-OCT-2003	(TREMBrel. 25, Last annotation update)		
TRYptophane hydroxylase.			
Mesocricetus auratus (Golden hamster).			
DOC			
Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Cricetinae;			
Mesocricetus auratus (Golden hamster).			
NCBI_TaxID=10036;			
RN			
SEQUENCE FROM N.A.			
Piarchinski A.V., Stolimski A.,	"Hamster tryptophan hydroxylase mRNA, complete coding sequence."		
Submitted (MAY-2001) to the EMBL/GenBank/DBJU databases.			
EMBL; AY034600; AK59708.1;			
GO; GO:0016597; P: amino acid binding; IEA.			
GO; GO:0005056; Furon ion binding; IEA.			
GO; GO:004510; Fltypophan 5-monooxygenase activity; IEA.			
GO; GO:0009072; Paracitramic amino acid family metabolism; IEA.			
GO; GO:0008152; Pmetabolism; IEA.			
GO; GO:0042427; Pserotonin biosynthesis; IEA.			
InterPro; IPR0123; Aaa-hydroxylase.			
InterPro; IPR002912; ACT.			
InterPro; IPR005983; Tyr_5_monomox.			
Pfam; PF00351; bipterin_H; 1.			
PRINTS; PR00312; PYHYDRXLAEB.			
PRINTS; PR003559; Aaa_hydroxylase; 1.			
TIGRFAMS; TIGR0120; TBPB_5' monoox.; 1.			
PROSITE; PS00367; BIOPERIN_H; 1.			
SEQUENCE 446 AA.; 51042 MW;	70B6ABB813E65352 CRC64;		
Query Match Score 12.3%; Best Local Similarity 24.9%; Matches 75; Conservative 47; Mismatches 112; Indels 67; Gaps 6;			
Qy 63 KCISLETPKANLFLV-----HILISKKNQREGG-----CST 92			
Qy 112 KKISDPLFCAVRMLYGSBDADHPGFKDNVRRRKYFAELLAMNYKHGDPIPKIEPTGE 171			
Qy 93 DMAVSTPFPNRNUMLYLRSRSPFLWIKSTCPRFELDYLAFGLSDFLH-----QA 144			
Db 172 EIKTMGTPTPFLNKLYPTAACR-----EYLRLPLISKYCGREENIPQIED 218			
Qy 145 VIKFEELTHFSYYPSVSGFVAAPHYQLSLQDRYPIASYMRTLDKDNFSLTPPLIHDLLG 204			
Db 219 VSNFLKECFSIRVAGLISPRFLSGAFRVNCTQVTRHSSDPLYTEPDTCHELG 278			
Qy 205 HVPWLHPSFSEFFNMGRFLTKVIEKVALPSKSKRQICLTQSNLIAVRCFWFTVBSGL 264			
Db 279 HVPLAEPSPAQFQSBDIG-----LSLGASEDVTYKLT-----CYPTVBERG 322			
Qy 265 IENHSGKAYAVNLSSPQELGHAFIDNTRVLPFLDQIIRLBNTSPOQELFSIRHFD 324			
Db 323 CKQDGQLRVFGAGLSSISLKLHSGAKVKPFDPKVACKQECCLITFQDVYFVSESFEE 382			
Qy 325 E 325			
Db 383 D 383			
RESULT 5			
QB71NO	PRELIMINARY;	PRT;	264 AA.
AC			
QB71NO; DT	(TREMBrel. 24, Created)		
01-JUN-2003	(TREMBrel. 24, Last sequence update)		
DT	(TREMBrel. 25, Last annotation update)		
01-OCT-2003	(TREMBrel. 25, Last annotation update)		
Phenylalanine-4-hydroxylase.			
Vibrionopsylviricus.			
OS			
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrio;			
Vibrionaceae; Shewanella.			
NCBI_TAXID=70863;			
RN			
SEQUENCE FROM N.A.			
RC			
STRAIN=MR1;			
MDLINE=22397686; PubMed=12368813;			
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,			
Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,			
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,			
Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,			
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,			
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,			
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,			
Muehlner J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,			
NCBI_TAXID=70863;			
RN			

Query Match 12.1%; Score 229; DB 16; Length 271;
 Best Local Similarity 26.3%; Pred. No. 1e-11;
 Matches 6; Conservative 49; Mismatches 113; Indels 20; Gaps 6;

Qy 93 DMDATVSTPFPENRNLWYRLISSRFSLWKSYCPRFLDYLEAFGILSDFLDHQAVI-KFFEL 151
 DR 18 DSGTHYPQBEHDWQLRQARQAVNLPGRACKYLQGDALANPKDLSIPQLAEIDKVLM 77
 DR 78 TTGKMKTADYPAISFGRFPELLANEKEPPATFRRKERFQDFLQEPDFHFGHCBLTN 137
 Qy 2112 PSFSEFFINGRGLRTKVIKVQALPSKCRQICLQSNLIAITRCFWTVESQLEINHECR 271
 DR 138 PSFAFHSMYNGOLGINA-----SKEDR-----VFLARLYWTVEPGLLKPKQE 181
 Qy 2772 KA-YGAVLSSPQQEIGHAIDNV-RVLPIPEDQIIRLDPLNTSPQETLTSIHPFDDELV 329
 DR 182 LCIYGGGILSSPGTLYAMESQVPERKFDDLVLRTRYRIDMOPIYYVIEHIDVDEI 241
 DR 330 TSKLEMW 336
 DR 242 -AKMDIM 247

RESULT 7
 Q8B8H3 PRELIMINARY; PRT; 263 AA.
 DR 08D650 PRELIMINARY; PRT; 263 AA.
 AC 01-MAR-2003 (TREMBUREl. 23, Created)
 DT 01-OCT-2003 (TREMBUREl. 23, Last sequence update)
 DE Phenylalanine-4-hydroxylase.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomondaceae; Pseudomonas.
 RN [1] _
 RN Sequence from N.A.
 RP STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
 RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AE016809; AAC07409.1;
 DR GO: GO:0005506; F:iron ion binding; IEA.
 DR GO: GO:0005505; F:phenylalanine-4-monooxygenase activity; IEA.
 DR GO: GO:0009072; F:aromatic amino acid family metabolism; IEA.
 DR GO: GO:0005559; P:phenylalanine catabolism; IEA.
 DR InterPro: IPR001273; Aaa hydroxylase.
 DR InterPro: IPR005960; Phenylalanine_H.
 DR Pfam: PF00351; biotin_independent_hydroxylase.

Query Match 12.0%; Score 226.5; DB 16; Length 262;

Best Local Similarity	24.9%	Pred.	No.	1.6e-11;
Matches	56;	Conservative	48;	Mismatches 104; Indels 17; Gaps 3;
106 LWYRLISSRFSLWKSICPRFFFLDYLBAFGGLSDFDPLHQAVI-KFPELETHESYYPPSGFV 164	Db	Qy	335 WMLDQCL 341	
26 VNTLITRQLKVEGRACQYDGDOLKLPHDRIVQLATGQVARVPALI 85	Db	Qy	241 AMVEIGM 247	
165 APHQYLSLQDRYPIASVMRTLDKUNFSLTDPDLHLDLGHVPWLHSSEFFINNGRL 224	RESULT 10	096370	PRELIMINARY;	PRT: 497 AA.
86 PDEOTPFPLASRKFPIVTPFLLQEDDIFIEPQGCPPLTNPWEPE-----137	Id	096370	PRELIMINARY;	PRT: 497 AA.
225 FTKVIEQVQALPSKPKQTQTLCSNLIAVRCEWTFESGLLENHEKRAKAVLSSPQE 284	AC	096370; 01-MAY-1999 (TREMBLrel. 10, Created)		
138 FTHTYQKLGLAATKEQRYV-----LARLYWMTIEFGLMETAQCRKIVGGILSSPQE 189	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
285 LGHAFTDNVRVPLPLEDDQIIRLFENTSTPQETLTSFRHDFEVEL 3.29	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
190 TVTSISDEPERQADFIEAMPFPPYDQPVYFLPNMKLFDL 234	DE	Tryptophan hydroxylase (EC 1.14.16.4).		
Schistosoma mansoni (Blood fluke)	GN	Tryptophan hydroxylase (EC 1.14.16.4).		
Eukaryota: Metazoa: Platyhelminthes: Trematoda: Digenea: Strigeida;	OS			
Schistosomatidae: Schistosomatidae: Schistosoma.	OC			
NCBI_TaxID:6183;	OX			
RN [1]	RN	SEQUENCE FROM N.A.		
STRAIN=Puerto Rican; PubMed=10419488;	RP			
MEDLINE=93348305;	RC			
Hamdan F.F., Ribeiro P.;	PA			
"Characterization of a stable form of tryptophan hydroxylase from the human parasite Schistosoma mansoni."	RT			
J. Biol. Chem. 274:21746-21754(1999).	RL			
EMBL; AF01034; AAD01923.1; -.	DR			
HSSP; P04177; 1TOH.	DR			
GO; GO:0005506: F:iron ion binding; IEA.	DR			
GO; GO:004510: F:tryptophan 5-monooxygenase activity; IEA.	DR			
GO; GO:0005072: F:aromatic amino acid family metabolism; IEA.	DR			
InterPro; IPR001273; Aaa hydroxylase.	DR			
InterPro; IPR005963; Tyr_5-monox.	DR			
PFam; PF00351; bioperin_H; 1.	DR			
PRINTS; PRO0372; FYNHYDRYLASE.	DR			
Prodrom; PD012559; Aaa_hydroxylase; 1.	DR			
TIGRFAMS; TIGR01270; Trp_5_monoox; 1.	DR			
PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.	DR			
KW Oxidoreductase.	KW			
SEQUENCE 49 AA; 57598 MW; F8964E4B4B2C361D CRC64;	SQ			
Query Match 11.9%; Score 224.5; DB 5; Length 497;				
Best Local Similarity 28.5%; Pred. No. 5.4e-11;				
Mismatches 34; Mismatches 108; Indels 29; Gaps 5				
Matches 68; Conservative 68;				
Qy 96 VISTPFPNRLWYRLLSRFSWPKVSYGKQVAPYHQLQDQYRPIASYMVRTLDKDNEFLTPDLDLHDLGHV 206	Qy			
Db 201 IVEYTELEKTWIGRIVRELTRLYKTSACHEF --QKNLGLQDKAGYNEFLPLQVQVS 256	Db			
Db 147 KPFELTHEFSTYPSVSGFVAPYHQLQDQYRPIASYMVRTLDKDNEFLTPDLDLHDLGHV 206	Qy			
Db 257 DFLKARTGFCLPVGAGLFLSGAFLRVYCTQVIRQADPYTPEPDQCHELIGHV 316	Db			
Db 207 PMILHPSFSEFFTMGRGLFTKVIEKQVQALPSKSKQRQTQLSNLIATYRCFWFTVEESGLI 266	Qy			
Db 317 PMADPKPFSQEQIG-----LASLGTSDEEKLAT-----CYFTTEFGFCR 360	Db			
Db 267 NHGGKAGAVLSSPQBLQHAFNDIVRLPFIELDQIRLPNTSTQETLSSIRHDE 325	Qy			
Db 361 QDNQKAYGAGLSSVAELQHALSKRAVIKPTIPMKVINEECVLTONGYFETSSPED 419	Db			
RESULT 11				
Q81LM9	ID	PRELIMINARY;	PRT:	584 AA.
OB1LM9	AC			
OB1LM9; 01-JUN-2003 (TREMBLrel. 24, Created)	DT			
OB1LM9; 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT			
Phenylalanine-4-hydroxylase.	DP			
216 BFFINMGRIFTKVIEKQALPSKSKQRQTQLSNLIATYRCFWFTVEESGLIENBEGRKAYG 275	216 BFFINMGRIFTKVIEKQALPSKSKQRQTQLSNLIATYRCFWFTVEESGLIENBEGRKAYG 275			
137 BFTTYQKGGLSA-----NKEQRYV-----LARLYWMTIEFGJVDTHGRRYIG 180	137 BFTTYQKGGLSA-----NKEQRYV-----LARLYWMTIEFGJVDTHGRRYIG 180			
276 AVLSSPQELGHAFDNTWRVPLFIELDQIRLPNTSTQETLSSIRHDE 334	276 AVLSSPQELGHAFDNTWRVPLFIELDQIRLPNTSTQETLSSIRHDE 334			

GN: BA4586. *Bacillus anthracis* (strain Ames).
 OS: *Bacillus*; Firmicutes; *Bacillales*; *Bacillaceae*; *Bacillus*.
 OC: Bacteria; Firmicutes; *Bacillales*; *Bacillaceae*; *Bacillus*.
 NCBI_TaxID:198094;
 RN: [1] *The genome sequence of Bacillus cereus and comparative analysis with*
Bacillus anthracis".
 RX: SEQUENCE FROM N.A. MEDLINE=2260B14; PubMed=12721629;
 RA: Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
 RA: Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA: Holtzapfel B.K., Oksstad O.A., Fouts D.E., Eisen J.A., Gill S.R.,
 RA: Go: GO:0005506; "Iron ion binding"; IEA.
 RA: Holzapfel B.K., Oksstad O.A., Holtzapfel B.K., Fouts D.E., Eisen J.A.,
 RA: Go: GO:0005506; "Iron ion binding"; IEA.
 RA: DeBoy R.T., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
 RA: DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA: Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA: Benton J.J., Mahamud Y., Hauck L., Hance J.R., Weidman J.F.,
 RA: Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA: Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
 RA: Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
 RA: Fraser C.M.;
 RT: "The genome sequence of *Bacillus anthracis* Ames and comparison to
 closely related bacteria.";
 RL: Nature 423:81-86(2003).

DR: EMBL: AE010102; AAP11265.1;
 DR: GO: GO:0005506; "Iron ion binding"; IEA.
 DR: TIGR: BA586.;
 DR: GO: GO:0005506; "Iron ion binding"; IEA.
 DR: GO: GO:0004497; F:monooxygenase activity; IEA.
 DR: GO: GO:0009072; P:aromatic amino acid family metabolism; IEA.
 DR: InterPro: IPR011273; Aaa_hydroxylase.
 DR: Pfam: PF00351; bioperl0.1.1.
 DR: PRODom: PDO02559; Aaa_hydroxylase; 2.
 DR: Complete proteome.
 SQ: SEQUENCE 584 AA; MW: 5610920323DFE89 CRC64;

Query Match Score 220.5; DB 15; Length 584;
 Best Local Similarity 23.5%; Pred. No. 1.5e-10;
 Matches 64; Conservative 51; Mismatches 112; Indels 45; Gaps 5;

Qy: 97 VSTPPF----NRNLYWRLSSRFLWVYCPRFPLDYEAFFGLLSDFLDHQAVIKFEE 150
 Db: 15 VSTQHNDQYTPVNHWAVRYLIMRQNSFLKDVAHAYVNGLOSSGNNID----AIPKVEE 69

Qy: 151 LE----THFSXPYPVSFGVAPHOYLSSLQDRYFPIASYVRTLDKDNFSLTPDLIHDLLGH 205
 Db: 70 MNECLAPSGLWAVTIDGLIGVAFDPFGHLPLATDIRKVENTEYTPADIVHEAGH 129

Qy: 206 VPWLHPSSEFFINMGRILPTKV1-----EKVQALPS -- 237
 Db: 130 APILLDPTAKVKGQGAKAFSTKEEDAEFVRTITIVESPTSTPDEVKAENAV 189

Qy: 238 KKQRJOTLQNLNIAVRCFEMTVESSLINHEGRKAYGAVLISSPQEQLCHAFIDNVRVL 296
 Db: 190 TEKQNLVSGLSAEQISRLFWTVXGLIGNIDDKRKYAGLSSVGESRHCLTDAVERKV 249

Qy: 297 PLEBDQIIRLFENTSPQETLFSRHFDELVE 328
 Db: 250 PESTEAGITGTYDVTMQPQLEVCSEEEETD 281

RESULT 13
 QPQZS
 ID: QPQZS
 AC: QPQZS
 PRELIMINARY:
 PRT: 296 AA.

Db: 70 MNECLASSGCAVTIDGLIGVAFDPFGHLPLATDIRKVENTEYTPADIVHEAGH 129

Qy: 206 VPWLHPSSEFFINMGRILPTKV1-----VIEKQALPSKKQ-----RIQTQLQSNL 249
 Db: 130 APILLDPTAKVKGQGAKAFSTKEEDAEFVRTITIVESPTSTPDEVKAENAV 189

Qy: 250 I-----AVRCPFMFTVYESGLINHEGRKAYGAVLISSPQEQLGHAFIDNVRVL 296
 Db: 190 TEKQNLVSGLSAEQISRLFWTVXGLIGNIDDKRKYAGLSSVGESRHCLTDAVERKV 249

OS: Xanthomonas axonopodis (pv. citri).
 OC: Bacteria: Proteobacteria: Gammaproteobacteria: Xanthomonadaceae;
 OC: Xanthomonas; Xanthomonadaceae;
 OC: Xanthomonas; Xanthomonadaceae;
 RN: [1] NCBI_TaxID:92822;

RN: SEQUENCE FROM N.A.
 RC: STRAIN=306 / ATCC 13902 / XV 101;
 RX: MEDLINE=2260B14; PubMed=12721217;

RA: da Silva A.C.R., Ferro J.A., Reinhach F.C., Farah C.S., Furian L.R.,
 RA: Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.P.,
 RA: Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA: Camarotte G., Cardozo J., Chambargo F., Ciapara L.P.,
 RA: Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA: Formighieri E.F., Franco M.C., Gregorio C.C., Gruber A., Ferro M.I.T.,
 RA: Faria J.B., Ferreira A.J.S., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA: Katsuyama A.M., Kishi L.T., Machado M.A., Martinec-Rossi N.M.,
 RA: Locali E.C., Martins E.C., Meidanis J., Menck C.Y., Moon D.H.,
 RA: Martins E.C., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA: Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA: Pereira H.A., Rossi A., Sena J.A.D., Silva C., Souza R.F.,
 RA: Spinola L.A.F., Takita M.A., Teixeira E.C., Tezza R.I.D.,
 RA: Trindade dos Santos M., Truffi D., Tsai S.M., White F.R.,
 RA: Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

RA: Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA: Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA: Grechkin Y., Busch G., Haselkorn R., Fonseca M., Erlich S.D.,
 RA: Overbeek R., Kyrpides N.;
 RT: "Genome sequence of *Bacillus cereus* and comparative analysis with
 RT: *Bacillus anthracis*";
 RL: Nature 422:87-91(2003).

DR: EMBL: AE010102; AAP11265.1;
 DR: GO: GO:0005506; "Iron ion binding"; IEA.
 DR: GO: GO:0004505; F:phenylalanine 4-monooxygenase activity; IEA.
 DR: GO: GO:0009072; P:aromatic amino acid family metabolism; IEA.
 DR: InterPro: IPR011273; Aaa_hydroxylase.
 DR: Pfam: PF00351; bioperl0.1.1.
 DR: PRODom: PDO02559; Aaa_hydroxylase; 2.
 DR: Oxidoreductase; Complete Proteome.
 SQ: SEQUENCE 584 AA; MW: 64223 MW; 5610920323DFE89 CRC64;

Query Match Score 220.5; DB 15; Length 584;
 Best Local Similarity 23.5%; Pred. No. 1.5e-10;
 Matches 64; Conservative 51; Mismatches 112; Indels 45; Gaps 5;

Qy: 97 VSTPPF----NRNLYWRLSSRFLWVYCPRFPLDYEAFFGLLSDFLDHQAVIKFEE 150
 Db: 15 VSTQHNDQYTPVNHWAVRYLIMRQNSFLKDVAHAYVNGLOSSGNNID----AIPKVEE 69

Qy: 151 LE----THFSXPYPVSFGVAPHOYLSSLQDRYFPIASYVRTLDKDNFSLTPDLIHDLLGH 205
 Db: 70 MNECLAPSGLWAVTIDGLIGVAFDPFGHLPLATDIRKVENTEYTPADIVHEAGH 129

Qy: 206 VPWLHPSSEFFINMGRILPTKV1-----EKVQALPS -- 237
 Db: 130 APILLDPTAKVKGQGAKAFSTKEEDAEFVRTITIVESPTSTPDEVKAENAV 189

Qy: 238 KKQRJOTLQNLNIAVRCFEMTVESSLINHEGRKAYGAVLISSPQEQLCHAFIDNVRVL 296
 Db: 190 TEKQNLVSGLSAEQISRLFWTVXGLIGNIDDKRKYAGLSSVGESRHCLTDAVERKV 249

Qy: 297 PLEBDQIIRLFENTSPQETLFSRHFDELVE 328
 Db: 250 PESTEAGITGTYDVTMQPQLEVCSEEEETD 281

RESULT 14
 QPQZS
 ID: QPQZS
 AC: QPQZS
 PRELIMINARY:
 PRT: 296 AA.

Db: 70 MNECLASSGCAVTIDGLIGVAFDPFGHLPLATDIRKVENTEYTPADIVHEAGH 129

Qy: 206 VPWLHPSSEFFINMGRILPTKV1-----VIEKQALPSKKQ-----RIQTQLQSNL 249
 Db: 130 APILLDPTAKVKGQGAKAFSTKEEDAEFVRTITIVESPTSTPDEVKAENAV 189

Qy: 250 I-----AVRCPFMFTVYESGLINHEGRKAYGAVLISSPQEQLGHAFIDNVRVL 296
 Db: 190 TEKQNLVSGLSAEQISRLFWTVXGLIGNIDDKRKYAGLSSVGESRHCLTDAVERKV 249

OS: Xanthomonas axonopodis (pv. citri).
 OC: Bacteria: Proteobacteria: Gammaproteobacteria: Xanthomonadaceae;
 OC: Xanthomonas; Xanthomonadaceae;
 OC: Xanthomonas; Xanthomonadaceae;
 RN: [1] NCBI_TaxID:92822;

RN: SEQUENCE FROM N.A.
 RC: STRAIN=306 / ATCC 13902 / XV 101;
 RX: MEDLINE=2260B14; PubMed=12721217;

RA: da Silva A.C.R., Ferro J.A., Reinhach F.C., Farah C.S., Furian L.R.,
 RA: Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.P.,
 RA: Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA: Camarotte G., Cardozo J., Chambargo F., Ciapara L.P.,
 RA: Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA: Formighieri E.F., Franco M.C., Gregorio C.C., Gruber A., Ferro M.I.T.,
 RA: Faria J.B., Ferreira A.J.S., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA: Katsuyama A.M., Kishi L.T., Machado M.A., Martinec-Rossi N.M.,
 RA: Locali E.C., Martins E.C., Meidanis J., Menck C.Y., Moon D.H.,
 RA: Martins E.C., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA: Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA: Pereira H.A., Rossi A., Sena J.A.D., Silva C., Souza R.F.,
 RA: Spinola L.A.F., Takita M.A., Teixeira E.C., Tezza R.I.D.,
 RA: Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

RA	Seubal J.C., Kitajima J.P.,	"Comparison of the Genomes of two Xanthomonas pathogens with differing host specificities",
RT		
RT		
RL	Nature 41:459-463 (2002).	
DR	EMBL; AE011641; AAH35066.1; -	
DR	GO: GO:0005506; F:iron ion binding; IEA.	
DR	GO; GO:0004505; P:phenylalanine 4-monoxygenase activity; IEA.	
DR	GO; GO:0009076; P:aromatic amino acid family metabolism; IEA.	
DR	GO; GO: GO:0006559; P:phenylalanine catabolism; IEA.	
DR	InterPro; IPR001275; Aaa hydroxylase.	
DR	InterPro; IPR005961; PhenylalanineOxidaseM.	
DR	Pfam; PF00351; bioperin_H; 1.	
PRINTS	PRO0372; FYWHDYKXLAEE.	
DR	ProDom; PDO02559; Aaa hydroxylase; 1.	
DR	TIGRFAMS; TIGR01267; Ph4hydrox mono; 1.	
DR	PROSITE; PS00067; BIOPTERIN_HYDROXYL; 1.	
DR	Complete proteome.	
KW	SEQUENCE 296 AA;	23467 MW;
SQ	288B1955670BC4BD CRC64;	
Query	Match Score 219.5; DB 16; Length 296;	
Best Local Similarity 27.9%; Pred. No. 7.5e-11;		
Matches 61; Conservative 39; Mismatches 82; Indels 37; Gaps		
Qy	126 FDLYEAFGLLSDFLDH-QAVIKPELEPHFSYYPVPSGEVAPHOYLSSQDYYFPIASM 1	
Db	60 FLQQAQDAMGNGQTHLPREFDALNRLVQAACTGWTLYVGQNLPLPDLFFDHLANTRFPVTTWWI 1	
Qy	185 RTLDKDNTSLSPDLTHLGHWPWLHPSESFEFINMGRFLTKVIEKYQALLSKKKQBIQT 2	
Db	120 RRPQDIDYTAEPDLPHDLCGHVPLMMNPFLADENQAYCR-----GGYKAHGIGGPDAQN 1	
Qy	245 IQSNLIAIVRCWFETVEGLIENHEGRKAYGAVLISS-----PQLGHAFTDN 2	
Db	174 L-----TRIWIYTFGLIDTPGQLRIGAVGIVSSKGESLSSPAPNRIG-----2	
Qy	293 VRVLPLEPDQIIRLPNTSTPQEQLSIRHDFELVELTS 3 31	
Db	221 -----FDLQRIMRTRYRIDSFQKTYFVIDSFQNLNEATA 2 54	
RESULT 14		
Q91WV1	PRELIMINARY; PRT; 453 AA.	
ID	Q91WV1	
AC	Q91WV1;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-Oct-2003 (TREMBLrel. 25, Last annotation update)	
DE	Phenylalanine hydroxylase.	
GN	PAH.	
OS	Mus musculus (Mouse)	
OC	BioCartia; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI-TaxID:10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-Kidney;	
RL	Straubberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DBJU databases.	
DR	EMBL; BC013458; AAH13458.1; -	
DR	MGI; MGI:19473; Pah.	
DR	GO; GO:0016597; P:amino acid binding; IEA.	
DR	GO; GO:0005506; F:iron ion binding; IEA.	
DR	GO; GO:0004505; P:phenylalanine 4-monoxygenase activity; IEA.	
DR	GO; GO:0003072; P:aromatic amino acid family metabolism; IEA.	
DR	GO; GO:0008152; P:metabolism; IEA.	
DR	GO; GO:0005559; P:phenylalanine catabolism; IEA.	
DR	InterPro; IPR001273; Aaa hydroxylase.	
DR	InterPro; IPR002912; ACT.	
DR	InterPro; PF01842; ACT; 1.	
DR	Pfam; PF00351; bioperin_H; 1.	
PRINTS	PRO0372; FYWHDYKXLAEE.	
>ProDom	PD02559; Aaa hydroxylase; 1.	

```

SQ* SEQUENCE 296 AA; 33232 MW; C2A4FE18B24B33DF CRC64;
Query Match 11.3%; Score 214; DB 16; Length 296;
Best Local Similarity 26.9%; Pred. No. 2.3e-10;
Matches 66; Conservative 44; Mismatches 97; Indels 38; Gaps 7;
Qy 126 FLDYLEAFGLISDFLDHQAVIKF-----PELETHESTSYPVSSGFVAPHQYQSLLQDRYFP 179
Db 60 FLOAQDAMG----MDDTQIPREFDALNATLQATGWTLLGVVEELLPELDFFDLANERFP 114
Qy 180 IASVNRILDKDNFSLTQDILHDLGHVPWLLHSFSEPFINNGRLFTKVIERVKQALPSK 239
Db 115 VTNWTRRPPQIDYIAEPDLFHDLFGHVPMLMNPFLADPMQAYGR----GGVKAHGIGP 168
Qy 240 QRIQTLSQNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSFOELGHAFIDNV-RVLPQ 298
Db 169 DALQNL----TRYWNTVEFLIAITQGLRYAGIVSSKGESLHSLESAPNFRVG 221
Qy 299 ELDQITIRLPNTSTQETLFSIRHDELVLTSLRQMLDGHLIESIPLY---NOEKYLS 355
Db 222 DLQRWMTRYRIDSQKTFVIDSFTQLNDAF-----DFTPIYAAIAQQQVP 271
Qy 356 GFEVL 360
Db 272 AGEVL 276

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Search completed: March 25, 2004 14:13:25
Job time : 47 secs